

FIGURE 1

ACTGCACCTCGTTCTATGATTGAACTTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGA
CCCCACGCGTCCGGGGCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTCCCG
CAGCGCTACCCGCC**ATG**CGCTGCCGCCGGCGCTGGGGCTCTGCCGCTTCTGCTG
CTGCTGCCGCCGGCGGCCAGGGCGCAAGAAGGCCGACGCCCTGCCACCGGTGCCGGGGCT
GGTGGACAAGTTAACCAGGGATGGTGGACACCGCAAAAAGAAGAACTTTGGCGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCCAGGAGGA
GCACCTGGAGGCCGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCCGAGGCCCTGCAGCGGAATGGCCACTGCAGCGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTCCACATGGGGTACCAAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCCGAACGAGACCCACAGCATTGACAGCCTGTGACGAGTCC
TGAAGACGTGCTCGGGCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCTGTGTGGATGTGGACGAGTGTGCGCCGAGCCGCTCCCTGACCGCTG
CCGAGTTCTGTAAGAACGCCAACGGCTCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTCTGACGGCTTCGAAGAACG
GAAGATGCCCTGTGTGCCGCCAGAGGGCTGAAGGCCACAGAAGGAGAAGGCCGACACAGCT
GCCCTCCCGGAAGACCTG**TA**ATGTGCCGACTTACCTTAAATTATTGAGAAGGATGTCC
CGTGGAAATGTGGCCCTGAGGATGCCGCTCTGCACTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTAAACAGCTGCATTCTTGGTTCTTA
AACAGACTTGTATTTGATACAGTTCTTGTAAATAAATTGACCATTTGTAGGTAATCAGG
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTGCACCTGCAGAACG
TTGGCCGCCATGGCCAACCTGTTATTGCACTTATAATGGTTACAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTTCACTGCATTCTAGTTGTGGTTGTCAAACACTC
ATCAATGTATCTTATCATGTCGGATGGGAATTAATTCCGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGGCGAAAGAACAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGAAAGTCCCAGCAGCTCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

>MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLPLLLLPPAPEAAKKPTPCHRRCRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEANWLQLKSEYPDLPFWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSRCRCHMGYQGPILCTDCMDGYFSSLRNEHTSICTACDESCKTCGTLNRDCGECEVGWVLDE
GACVDVDECAAEPPCSAAQFCKNANGSYTCEECDSVGCTGEGPGNCKECISGYAREHGQCADVDEC SLA EKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEAATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CGAGTCCAACTGCACCTCGGTTCTATCGATTGAACTCCCGGGATCCTCTAGAGATCCTC
GACCTCGAACCCGGCTCGCCAGGGCGGGAGCAGCCGGCCACCGCTCTAAACCGGAAACA
GCCCCTGGCTGAGGGAGCTGCAGCAGCAGAGTATCTGACGGCGCAGGGTGCAGTGGC
GCACGAGGAGTTTCCCGCAGCGAGGAGCTCTGACCGAGCATGGCCAGCAGCAGCAG
CTCTGGCCCGCGCTCTGGCTCTGAGCATCCTCTGTGCTGCTGGACTGCGGGCGAGGC
CGGGCCCGCAGAGGGAGGAGCAGCTGACCTATGGATCTGATGGCTCAGCAGGAAGAGTACTCA
TAGGATTGAGAAGAGATATCTCTGATTGTTCTAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCGCAGCTATTCTCTGCAATATCCATCTGAAATTTCAC
CTGGCAAGCTGCAGGGCAGGAGAAATACCTCTATGAACTTCTGCTCTGGCTCCCTGATA
AAGGCATCATGGCAGATCACAACCGTCATGTCCTCTGCTGGAAACAGTGCCTCAACAGGC
TCAGTTCTCAAGTGGTTTCTCATGCTCTGGAAAACAGGATGGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAACTCTGAAAGGCAACACCACTTCTCAAACACCTCAAATGCTATCT
TCTTTAAAACATCTCAACAGCTGACTGCTCCAGGGCGGTGCGGAAATGGAGCTTTTGTAAAT
GAAAGACCATCTCGAGGTGCTCTGATGGTTCTCAGGGACCTCAGTGTGAGAAAGCCCTTGG
TACCCACGATGATGAACTGGTGGACTTTCTGTGACTCTGGTTCTGCATCTGCCAACCTG
GATTCTATGGAGTGAACGTGACAAAGCAAACCTGCTCAACCACTGCTTAAATGGAGGGACC
TGTTCATCCTGGAAAATGTTGCTCTCAGGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCAACACCTGCTGAAATGGAGTAAATGCTATGGTAAAGAACATGTAAGTGGT
CCAAAGGTTACCAAGGGAGACCTCTGTTCAAAGGCTGCTGCGAGCCTGGCTGTTGACAT
GGAAACCTGCATGAAACCCAAACATGCAATGTCAGAAGGGTGGCATGGAAGACACTGCA
TAAAAGTACGAAGCAGGCGGACTCATACATGCCCTGAGGGCAGCAGGCCAGCTCAGGCC
ACACGCCCTCACTAAAAGGGCAGGAGCGGCCGGGATCCTGAAATCAATACATCTGG
TGAACTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTCTAGCCTTGTAAACCTTCA
TGTGTGTAAGTTCAAAATGTTCTATCACCTAAAGGAAATCTGGCTGAAATTTTATTAGCT
TCATTAATAATCACTGAGCTGATATTCTCTCTTAAAGTTCTTAAGTACGTCTGAG
CATGATGGTATAGATTCTTCTGTTCTAGCTTGGGACAGATTTATATTGTCATTTGTA
CTGCTTTAAAATTTCTGAGTGTGAGTGGCAGATATTCTAAAATTCAATGCAATTATGGT
GTCTGGGGCAGGGAACTCAGAAAAGGTTAAATGGGCAAATGCTGAAAGTCAAGAAT
TTGGATGGCTGAGCTTAAATGTAAGTTACAGCATTCTGAGATTTTATTGAGCATGATTTAGAT
GTTTGTGATCATTTTAAAATGCTCTTAAATTAAACTCTCAATACAATATATTGAC
TTACCATTTCCAGAGGAGTCACTGATTTAAATTTAAACTACTGCTGAGTGGCATT
AAACATATAATATATTCTAAACAACTGAAATAGGAAATATAATGTAAGTGAACCTTGT
TGGCTGAAAGCAATATAATATTGTAACAAAACACAGCTCTTACCTAAATAACATT
ACTGTTGTGATGTTAAAGGTGCTGCTTCTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGACTCGACCTGAGCTGAGCTG
CGCCATGGCCCAACTTGTGTTATTGCGACTTAAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQABYFYEFSLRSLDKIMADPTVNVP LL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICCECPDGFHGPHECEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGK CICPPGLEGEQCEISKCPQPCRNGGK CIGKS KCKCSKG YQGDLC SKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACCGCGTGGCGTCCGGCGTCGAGAGGCCAGGAGGCCAGGCCAGGAGGCCACCATGGCGATGTCCACTGGGCTAC
TGGCTGTTGCTGGCGCTGGCTGCCACTTGGCTCTGGGTGCCAGCAGGGCTGAGGGCTGAGGGCCGG
GAGCTAGCACGGGCTCTGCACCTGCGGGGATCCGGGACGGCAGCTGTGCCCTGCCACTCTGGGCGCATT
GCAGGACCTGTGCTGCCGGCGTGGCGACGACTGTGCCCTGCCACTCTGGGCGCATT
GTTACTGTGACCTCTTGTGCAACCGCACGGTCTCGACTGCTGCCCTGACTCTGGGACTTC
TGCCTGGCGTGGCCACCCCCCTTTGGGATCAAGGATGTATGCGATGGAGGTGCTATCTA
TCCAGTCTGGGAACGTACTGGGACAACGTGAACTGGCACTGGCAGGGAAACAGGAGT
GGCATGGTGGATCCAGACATGATCAAAGGCAATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACACAGGCCCTCTGGGCATGACCTGGTGAAGGGCATTGCTAACCCCTGGGACCA
TCCGCCATCTTCTCGTGAACATGCAATTATACAGTGTGAACCCAGGGAG
GTGCTTCCCACGGCTCTGAGGCCACTGAGAAGTGGCCAACCTGATTGATGAGCCTCTTGA
CCAAGGCAACTGTGCAAGGCTCTGGGCTTCTCACAGCACGTGTGGCATCCGATGTGCT
CAATCCATTCTGGGAACATGAGCCTGTCTGCGGGAGAACCTGCTGTCTGGAC
ACCCACAGCACAGGGCTGCCGGTGGCTCTGATGGTGGCTGGTCTCTGGCTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTGGGGCTGAAAGAGACGAGGCTGGC
CTGGCCCCCTGTATGATGCAACAGCGAGGCTGGGTGGGGCAAGGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAAACATGACATCTACAGGTCACTCTGTCTACGCCCT
CGGCTCAACGACAAGGAGATCTGAAGGGCTGATGGAGAAATGGCCCTGCTCAAGGCCCTCA
TGGAGGTGCATGAGGACTTCTCTATACAAGGGAGGCATCTACAGGCCACAGGCCAGTGGC
CTTGGGAGGCCAGAGGAGATCACGGCGCATGGGACCACTCAGTCAAGATCACAGGTGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAAATCTGGACTGCCCAACTCTGGGCC
CAGCCTGGGGCAGAGGGCACTTCCGATCTGCGCGGCCAATGACTGCGACATCGAG
AGCTTCTGCTGGCGCTGGGCTCTGGGCGCTGGGATGGAGACATGGGTATCACTGAGGCTG
CGGGCACCCAGCGGGTCTGGGCTCAGGATCAGGCTAAGGGCCGGGAAGAGGCCCAATG
GGGGCGTGAACCCAGGCCCTGCCAGACAGGCCGGGCCAGCGGGGCCAGGGCTAAT
CCCGCGCGGGTCTCGCTGACCGACGCCCGCTGGAGGCCGGCAGGCGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGACGGGGCAGGGCTGGGAAGAGCACAGCTGCAG
ATCCAGGCCCTGGCGCCCCACTCAAGACTACAAAGGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTTCTTTTTTTTTAGACAGGGCTTGTCTCCG
TTGGCCAGGTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCACTCTGGGTCA
ATGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCCACACCTGGC
TAATTTTTGTATTTTTGTAAGAGGGGGTCTCACTGTGTTGCCCAGGGTGGTTCAACT
CCTGGCTCAAGCGGTCCACCTGCCCTGCCCTCCAAAGTGTGGGATTGCAAGGATGAGCC
ACTGACCCAGGCCCTGTATTCTTCAAGATATTATTTTCACTGTTTCACTGTTTAAAA
TAAACCAAGTATTGATAAAAAAAA

FIGURE 6

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHIALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCRGRADD
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
```

N-glycosylation site.

amino acids 78-82, 161-165

 **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

 **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

 **Amidation site.**

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTCTGTGTCTCAAATCCA
ATTCTCTGGACACATNACGCCCTGCTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCGCCAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCG
CCCCCTGTATGATGCACAGCCGAGCCATGGTCCGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTCTTCCATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGG
GAGCAGTGCCTGACCGCGCGCATCGCGCAGTGGCCTCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACCTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCTGCTGCTGGGACCCGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTTGCCCCAGGCCTCTGCCCCACTCCTCACAGACCTG
GCCCAAGTGGGAGCCTGTCCTGGTCACTGAGGCACATCCTAACGCAAGTGTGACCATGTATGT
CTGCACCCCTGCCCCACCCCTGACCCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGCACACAGATCCGCTGCAGATGGCCCTCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCTGTGCTCAGGACACCTCTTCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGG
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAPFSTLNPVLRHLFPQEAFPAHPITYDLSQVWSVSPAPSRRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

 **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

 **N-myristoylation site.**

amino acids 56-60

 **Amidation site.**

amino acids 70-74

FIGURE 10

CCACCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTACCCGGCGTCCATCTCCGCCACCGCGAGGACGGCAACAAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCGGGTTGTCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGAAGAGCAAAGACTG
CGTGGTCACGGAGATCGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGCCCTCACGGCGAGGGCGCCCGCCAGGCTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACAGAACAGCTTCAGTTGTGGCTCCGCCAACCGCCGGACCAAGCGCACAC
GGCGGCCAGCCCCCTACGTAGTCTGGGAGGCAGGGCGAGCAGCCCCCTGGCCGCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCGCGAACATCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGCTGGCACAGTGCCCCCTCCCGACGGGTGGCAGGCCCTGGAGAGGAACCT
GAGTGTCAACCTGATCTCAGGCCACCAAGCCTCTGCCGCTCTCCAGGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCTTGCAGACAAACCGTCTGGAGGTGGCTGTCCTAAAA
TCTGCTTCTCGATCTCCCTCAGTCTGCCCCCAGCCCCAAACTCCTCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATCCACGACCAGGCCTGCACCCACCCAACTCCAGCCC
CGGAATAAAACCATTTCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPGSKDCVFTIEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEEF
VGSAPTRRTKRTTQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGAAAAAATTCTCCCTGTTGAATTTCGGCACATGGAG
GACAGCAGCAAAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATAGCCCTCACGGACGTTCTCTAGCTGAGTTCTGGACTCTCAACAGAACCCCATCCAGT
CATTTTGATTTGCTGTTTATTTTCTTTCTTTCCACACATTGTATTATTTAT
TTCCGTACTTCAGAAATGGCCTACAGACCAAAAGTGGCCAGCCATGGGCTTTTCCT
GAAGTCTTGCTTATCATTTCCCTGGGCTACTCACAGGTGTCACACTCTGGCTGCC
CTAGTGTGCGCTGCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTGGGATCCCGGAGGGCTAACCGTACTCTACCTCCACAAACAAACAAATTAAATAGC
TGGATTCTCGAGAACCTGACAGTCTGGTCAACGGTCTACCTGTATGCCAAC
AACTGGACGAATCCCCATGAACCTTCCAAGAACATGTCAAGAGTTCTCCATTGCAAGAAAAC
AATTACGACCATTCACAGTGGCTCTGGCAGCTTGAAGAGCTTGACACCT
GGATGACAACCTCCATATCCACAGTGGGGTGAAGAGCAGGGCCTTCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTGGCTTCTGTGGAC
TTCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTATCCGACATGGCCTTCAGAA
TCTCACGAGCTGGCGTCTATTGCGACAGGGAACCTCTGACCAAAAGGGTATCGCCG
AGGGCACCTTCAGGACATCTACCAAGCTAACGAAATTCTAATTGTACTGAATTCCCTGTC
CACCCCTCCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCCAGAT
AAACACCATCCCTTGACAGCCTCTCAAATCTGTAAGCTGGAAACGGCTGGATATATCCA
AAACACCAACTGGGATGCTGACTCAAGGGGTTTTGATAATCTCTCCAAACCTGAAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGTGACTGAGTATTAAATGGGTACAGAATGGCTCAA
ATATATCCCTTCATCTCAACGTGCGGGTTTCTGTGCAAGGCTCTGAACAAGTCGGG
GGATGGCCGTAGGGAAATTATGAATTCTTGTCTGTCCACACAGGACCCCCGGCTG
CTCTCTTCAACCCAGCCCCAGTACAGCTTCTCGGACACTCAGCTCCACCCCTCTAT
TCCAACCCCTAGCAGAGCTACACGCCCTCAACTCCTACACATCGAAACCTCCACGATT
CTGACTGGGATGGCAGAGAAAGCTGACCCACCTTCTGTAACCGGATCCAGCTCTCTATC
CATTGTGAAATGATACTTCCATTCAAGTCAAGTCTGGCTCTCTCTCACCGTGTGGCATA
CAAACTCACATGGGTGAAAATGGCCACAGTTAGTAGGGGGCATGTTCAAGGAGCGCATAG
TCAGCGGTGAGAAGAACACCTGAGCTGGCTGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTCAGTGCCTACTGGATGCTTTAACTACCGCGGGTAGAAGACACCCATTGTTCAAGAGC
CACCAACCATGCTCTCTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGCGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGGGCTTGATCGGGGGCGCGGTGATATT
GTGCTGGTGGTCTGCTCAGCGTCTTTGCTGGCATATGACACAAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATAACACGGGGCGCGGAAAGATGATTATTGCGAGGCAGGACCAAGA
AGGACAACCTCCATCTGGAGATGACAGAAACAGTTTCAGATGTCCTTAAATAACGAT
CAACTCTTAAAGGAGATTTCAGACTGCAAGCCATTACACCCCAAATGGGGCATTAATT
CAAGACACTGCCATATCCCCACAAACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGGGACAATTAGACTCTTGAGAA
CAACTCGTGTGACATAAAGACACGCAAGATTACATTGATAAAATGTACACAGATGCAT
TTGIGCATTGAAATACTCTGTAATTIATACGGTGTACTATATAATGGGATTTAAAAAGTG
CTATCTTCTATTCAAGTTAACTACAAACAGTTGTAACTCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPSPHGAFFLKSWLIIISLGLYSQVS KLLACPSVCRCDRN FVYC NERSL TSVPLGIP
EGVTVLYLHNNQINNAGFP AELHN VQSVH TYLYG NQ LDEFPMN LPKNVRVLH LQENNIQTI
SRAALAQLLKLEELHLD DNSI STVGVEDGAFRE AISL KLLFLSKNHL S SVPVGLP VD LQ ERL
VDENRIAVISDMAFQNLTS LERLIVDGNLLTNKGIA EGTFSHLTKLKEFSIVRN SLSHPPD
LPGT HLR LRLYLDNQINH IPLTA FSNL RKL ERLD ISNNQ LRM L TQGVFDN L S NL KQ L T ARNN
PWFCDCSIKWVTEWLKYI PSSL NVRG FMC QGPEQ VRGM A VRE LNM NLLS CPTT PGLPL FTFP
APSTASPTIQPPTLSIPN P SRSYTPPPTSKLPTI PDW DGRERVTPP I SERIQLS I HFVND
TSIQVSWL S LFTV MAYKLTWVKMGHSLVGGIVQERIVS G EKQHLSL VN L EPRSTYR I CLVPL
DAFNYRAVEDTICSEATTHAS YLNN GNTASSHE QTTSHSMGSFLLA GLIGGAVI FVLVVL
LSVFCWHMHKKGRY TSQKWK YNRGRRK DDYCEAGT KKD NSI LEMT ETSF QI VSLNN DQLLKG
DFRLQPIYTPNCGGINYTDCHI PNNM RYCNS SVPD LEH CHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300, 522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHWPQTALLESSCENKRADLVFIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTDRVGLLQGSTVKEFSLKTFKRKSEVERAKRMRHLSTGTMGLAIQYALNIAFSEAEAGRPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIVGVQVDFNTLKSIGSEPHEDHFLVANFSQIETLTSVQKCLCTAHMCSTLEHNCAHFCINIPGSYVCRCKQGYILNNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEDEGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINYCALNKPGCEHECVNMEESYYCRCHRGYTLDPNGKTCRSVHDCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTCSRVDYCLLSDHGCHEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCEHSCVSSEDSFVCQCFCFGYIILREDGKTCRRDKVCQAIHDGCEHICVNNSDSDSYTCBCELEGFRLAEDGKRCRKKDVCKSTHGCHEHICVNNGNSYIKCKCSEGFGVLAEDGRRCKCTEGPIDLVFVIDGSKSLGEENFEVVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRRNFNSAKDMKKAVAHKYMGKGSMTGLALKHMFERSFTQGEGAPRLSTRVRPAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIKEELQEIASEPTNKHLYFAEDFSTMDEISEKLKKGICEALEDSDGRQDSPAGELPKTVQQPTSEPVTIQIDQLLSCNSNFAVQHRYLFEEDNLLRSTQKLSHSTKPGSPLEEKHDQCKCENLIMFQNLANEEVRKLTQRLLEEMTQRMEEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTGGCTCCCGCGCACGCTCCGGCCGCGCAGCCCTG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTCCCTCCCGGGCCCTGGTACCCAACTTGCTCGGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCGCCCTCGCGGGCCAGCTGCAACTGCACCTGCCGCAACCGGTTGAG
GCCGTGGAGGGAGGGAAAGTGGTCTTCAGCGTGGTACACCTTGACCGGGAGGTGCTTC
ATCCCAGCCATGGGAGGTGCCCCTTGTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAAACAAGCAAACCTGGAGTATCCTGGTACTCC
ATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGTCCTGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCTCATCTGCCGTCTCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCAGTCTCAAGGAGTAAGCCCGTGTCAAATACCA
GTGGGATCGGCAGCTTCCATCTTCCAGACTTCTTGACCCAGATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCAGGCCCAC
AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGGTACCTGGTGTGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCAACCGCCGGGCAAGGCCCTGGAGGAGGCCAGGAAATGATACTAAGGAGGATGCC
ATTGCTCCCCGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAAATGGGACCC
TTCCCTGTACCTCCGCACGAGCCCTCGGCCACCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGCTCTCCAGGCCAGGGCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCACCCCAACCAATCCCCATCCCTGGGGTTCTTCCCTGGCTTGAGCCG
CATGGGTGCTGTGCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**TGATGAC**
CCCACCACTATTGGCTAAAGGATTGGGTTCTCTCCCTATAAGGGTCACCTCTAGCAC
AGAGGCCCTGAGTCATGGGAAAGAGTCACACTCCCTGACCCCTAGTACTCTGCCCCCACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAAGGAGAAAGGAA
AGTGGATCTGGATTGGGAGGAGCCTCCACCCACCCCTGACTCTCCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTCTGAGCTCCAGGC
CCCCCTGATCTGATCCCCACCCCTATCTAACACCACCTTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTAGGTTACTGGGAGAGGATAGGGATCTC
TTATTAACATGAAATATGTGTTTCATTGCAAATTAAATAAGATAACATAA
TGTGTTGATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNSSMAGVYVCKAHNEVGTAQCNVTLLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEADAIAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCCTCCGCTCCTAGTGGTTTTCCACTTG
TTGAATTGTCCTATACTCAAATTGCAACAGACACCTGTCTCCAAATGCAAATGTGA
AATACGAATGGAATTGAGCTGCTATTGCAACATGGGATTTAGGAAATGGTGTACAA
TTTGTGAAGAGTATACTGAATGTTGAAATTAACTCACTCTGTGGCAGAAATGCTAATTG
ACTAACACAGAAGGAAGTTATTGTATGTGCTAGTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTACTAATGATGGAACCTCTGTATAGAAAATGTAATGCAAACGTGCAATT
TAGATAATGTCGTATAGCTCAAATATTAAACAAAATCTTACAGATCCACCAACAGA
GAACCTGTGGCTTGTACAGAAGCTATACTGAGAATCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATATTAGCTGAATCATCTTCAACTAGGTTAACAGAACACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGTAACCGTGAAT
AATTGTCCTAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTCAAAACTCATGCACACTGTTGACAAGCTTTAAGGATATCCCGAGAGCTTCC
AAAAGACCAAGAGTTGTACAAATTCAACGGATATAGCTCTCAAAGTTTCTTGTGAT
TCATATAACATGAAACATATTCTCATATGAATATGGATGGAGACTACATAAAATATT
TCCAAAGAGAAAAGCTGATGATGCAATTGCAATGGCAATTGCAATTGCAATTGTAATT
AGAGTATTGGCTCTTGTCTTCATCTGACAATTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGGAGAAAGGTATCATATCTCAGTAATTCTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATGAACTTGTGAAAAAAATACATTACATTAACTGATCATGAAAGGTACAGATA
GGTATAGGAGTCTATGTCATTTGGAAATTACTACCTGTGATACCTGATACCTGAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACCTCTCATGCCGTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGTCCTTCCATTGGTATTAAAGATTATAATATT
TTACAAGGGATCACTCAACTGAAATTATTCTACTGATTGTTGCTTGCATTTTGCATT
ACCTCTGGTTCTTCAGTGAATTCAAGGCCACCGAACAACTTCAAAAATCTTGTG
TAGCCTATTCTGCTGAATTGTTTCTGTTGGATCAATACAAATACTAATAAGCTCT
TCTCTTCAATCTGGCGGAGTGCACACTACTCTTTTAGCTGCTTTGATGGATGTGC
ATTGAAGGCATACTCTCATCTCATTTGGTGGGTGTCATCTACAAACAAGGGATTGCA
CAAAGATTTTATATCTTGTCTATCTAACGGCCAGCCGTGGTAGTTGGATTTCGGCACAC
TAGGATACAGATTATGGCAACCAAAAGTATGTTGGCTTAGCACCAGAAACACTTTATT
TGGAGTTTATAGGACAGCAGTCCTAACTCATTCTGTTAATCTTGTGCTTTGGAGTCAT
CATATACAAAGTTTCTGCACACTGCAAGGGTAAACCAAGGAAAGTTAGTTGCTTTGAGAAC
TAAGGTTCTGCAAGAGGAGCCCTCGCTCTTGTGTTCTCTCGGCACACCTGGATCTT
GGGTTTCTCCATGTTGTCAGCCTAGTGGTTACAGCTACCTCTTCAAGTCAGCAATGC
TTTCAGGGATGTTCTCATTTTTATTCTCTGTGTTTATCTAGAAAATGTCAGAACAGAT
ATTACAGATTGTCAAAATGCCCCCTGTTGTTGGATGTTAAGGTAAACATAGAGAATG
GTGATAATTCAACACTGCACAAAATAAAATCCTGAAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTCTCAATTAACTACTAGACAAAAAGTATTAAATCTAGTTTCT
GTTTGTCTATGAGACTGTAGATAAAAGTAAATTATGATCATATAGATACTATGT
TTTCTATGTGAAATAGTCTGCAAAATAGTATTGAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCATGCACCCAAAGGAAGATTCTTCTAACACAGAGAAGTATGAA
TGTCTGAAGGAACACTGCTGTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACCACTCGGTAAATGAGCTCATTACAGAAAAGTGGACACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAGGGAGTGTAAAGATGTATTGAAATGAAACTGTTTACCTTTGTGAA
TAGCTGAGAAATTGTTGACATAAAACACTTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTTACCTCCACAAATTGAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCNTTEGSYCCMVCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNVIAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTL
SNSTLTERFVKTVMNFVQRDFTVWWDKLSVNHRRTHLTKLMHTVEQATLRLISQSFQKTTEDFT
NSTDIALKVFFFDSYNMKHIHPHNMNDGYDVINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPKQNYDNSEEERVISSVISVMSNPPPTLYELEKITFTLSHCKVTDYRSLCAF
WNYSPDTMNGSWSEGCELTYSNETHTSCRCHNLTHFAILMSSGSPSIGIKDYNILTRITQLG
IIISLICLAIICIFTFWFFSEIQRSTTIIHKNLCCSFLAELVFLVGINTNTNKLFCSIIAGL
LHYFLAFAFWMCIEGHIYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVVGFSAAALGYRYYGT
TKVCWLSTENNFIFWSFIGPACLIILVNLLAFGVIIYKVRHAGLKPVCFCENIRSCARGA
LALLFLLGITWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGGCGCTGCGCGGTGGGGAGGAGTTCCCGAAACCCGGCG
CTAAGCGAGGCCCTCCTCCCGAGATCCGAACGCCCTGGCGGGGTCAACCCGGCTGGGA
CAAGAAGGCCCGCGCTGCCCTGCCGGGCCGGGGAGGGCTGGGGCTGGGCCGGAGGCC
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGTATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCCACTACCCGTGGGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCCGCGCGCGCTCAGAGCAGGCCTGCCCTCAGGATCTAGGGCCACGACCATCCAAACCC
GGCACTCACAGCCCGCAGCGCATCCCGTGCCTGCCAGCCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCA**AT**TCGGAGCGGTGTGTGGGGTCAAGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGCTGGCGGGGGCGCCCTTCGCGGCACCTGTACACCTCCGGGGCC
CCACGTGCACTACGGCTGGGGCACCCATGCCCTGCCGCGCACTGTACACCTCCGGGGCC
ACGGGCTCTCAGCTGCTTCTGCCATCCGTGCCAGGGCTGTTGGACTGCCGGGGC
CAGAGCGCGCACAGTGTGAGGAGTCAAGGCGACTCGCTCTGCCGGACCGTGGGACATCAAGGG
CGTGCACAGCGTGGCGTACCTCTGCATGCCGCCAGGGCAAGATGCAAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGTTCTGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCGGAGAACGCTCCGGCTCCCGTCTCCGTGAGCAGTGCACAAACAGCGGCAGCTGACAAAGAA
CAGAGGCTTCTTCACTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGGAGCTG
AGGACACTAGGGGCCACTTGGAAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTACCGGACTGGAGGCCGTTGAGGAGTCCCAAGCTTGTAGAA**ACT**
GAGACCATGCCGGGCTCTTCACTGCTGCCAGGGCTGTGGTACCTGAGCGTGGGGGAGC
TGCTTCTACAAGAACAGTCTCTGAGTCCACGGTCTGTTAGCTTAAAGAAAATCTAGAA
GTTGTACATATTCAAGGTTTCAATTGGCAGTGCCTAGGCAATAGACTGTCTGAT
CTAAACATCTGTAAGCTGTAGCTGCCAGCTGCTGCCGGGGCCCATCTGCTCCCTCGA
GGTGTGTCGACAGCTGCTGCACTGCTCAAGTCTGCTGAGTAACTCCATCGATGGGAAC
TCACTTCTTGGAAAATTCTTATGTCAGCTGAAATTCTCTAATTCTCATCATT
CCCAAGGAGCAGCCAGAACAGCAGGAGTATTAAATTCAAGGAAACAGGTGATCCACTCTGTA
AAAAGCAGGTAATTCTCACTCAACCCCATGTTGGAAATTGATCTATCTACTTCCAGGG
ACCAATTGCCCTCCAAATCCCAAGGCCAGAACACTGACTGCCAGGAGCAGCATGGGCCAACAG
GCCTCAGGAGTAGGGGAAGCTGGAGGCCACTCCAGCCCTGGGACAACCTGAGAAATTCCC
CTGAGGCCAGTCTGTCATGGATGCTGTCTGAGAATAACTTGTGCTGCCGGTGTCACTG
TTCCATCTCCGCCAACAGGCCCTGCCACCTCTGCTGCCAGTGCCTCCCATGGATTGGGCC
CCCAAGGCCCTCCACCTTATGTCACCTGCACTTCTGTTAAAAATCAGGAAAAGAAAAGAT
TTGAAGAGCCCCAAGTCTTGTCAATAACTTGTGCTGAGCAGGCCGGGGAGACCTAGAAC
CCTTTCCCGACACTTGTCTTCAACATGATATTATGAGTAATTATTGTATGTACA
TCTCTTATTCTTACATTATTATGCCCCAAATTATATTATGTAAGTGAAGGTTTG
TTTGTATTAAGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEET
EIRPDGYNVYRSEKHRLPVSLSSAKQRQILYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCAGAAGTTCAAGGGCCCCGGCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCGCGCTGCCGCCGGGAAAGATGGCGAGGAGGAGCCGCCACGCCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTAGCCTGCAAACCCAA
AGAAGACTGTTCCCTCAGATTAGAGTGGAAAGAAACTGGTGGAGTGTCTCCTTGCTAC
TATCAACAGACTCTCAAGGTGATTTAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGCGGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCAGTCTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTCTGCTGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGATCCAGCTCTGAATACACATGGTTAAGGATGGCATCGTTGCTAGAAA
ATCCCGAGCTGGCTCCAAAGACCAACAGCTCATACACATGAATAACAAAAACTGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAAATTCCCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAGGCTACTTTCAAAAGAAACCTCCTTCAGAAGAGTAATTCTTCATCTAA
ACCCACGACAATGAGTGGAAAATGTGCACTGGCTCACGCCCTGAATCCAGCAGTTGGAGG
CCGGGGCGGGCGGATCAGGAGTCAGGAGTTCAGACTGGCAATATGGTGAACCC
CATCTCTACTAAAATACAAAATTAGCTGGCATGGGGATGTGCCAGTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAACTGAACCCGGAGGCGGAGGGTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAAACAGAGCAAGATTCCATCTCAAAAAAATAAAATAAAATA
ATAAAATACTGGTTTACCTGAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAIACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGINNPLGSQST
NSSYTMNTKTGTQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIIAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGAGCAGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCACAGCCGGACCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAACATGGGATTAAATATTCTACTCAAATAA
ATGAATTACTCAATCTCTATGACCATCTACACTCACCCTCAAAGTACATCAAATA
TTATATCATTAAGGAAATACTAACCTTCTCTCAAATATGCATGACATTGGACATG
CAAATTGTGGCACTGGCACTTTCAGTGAAGAAAACATTGTGTTCTATGGCATTCA
TTTGACAATGCAAGCATTCTCTTATCAACTCAGGCTCTATTGAACCTACTAGCACTGACTG
TGGAAATCCTTAAGGGCCCATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGCTACTTGGCCTAGCTATCACACTAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTAGTGTGAAATCAGGCCGGTTACACCCAGATCCATTAT
ATGGAAGCATTCACTAGTGGATTGTAAATGATTAGGCTCTTAACTTTCCAGGCCAGATTGCC
AGCTAACACACAGATTCTCTCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGCCCTGGATTATCTCAAACAAATTTATCTCAGTCAAAAT
ATTAAATGTAAAAGATGCCCTAGCTCTTCTGTGTACTAGAGGAAAACAAACTTACTGA
ACTGCTGAAAATGTGCTGCGAACATGAGCAACTTACAAGAACACTTATAATCAAACACT
TGCTTCTACAAATTCACTGGGCCATTATTGGCCATACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAAGTGTCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCTAAATTATGCAAGAACAGCATGAACTTTAAGCCTCTTATCA
ATCTTGGCAGCTGGTTATAGCTGGTAAACACTCAGAACATACCGAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAGAACATCTTTTACGATAACAGGCTTATAAAGTACCCATGT
TGCTCTTCAAAGTGTGAAATCTCAAATTGGATCTAAATAAAATCTTAAATAGAA
TACGAAGGGGTAGTTTACCAATATGCTACACTTAAAGAGTTGGGATAAATAATATGCC
GAGCTGATTTCATCGATGACTTGTGCTGGATAACCTGGCAGATTAAAGAAAATAGAAC
TACTAACACCTAGATGTTCTTACATTCAACCCCAATGCACTTTCAGACTCCCAAGCTGG
AATCACTCATGCTGAACAGCAGCAATGCTCTGGCCCTGTACCATGGTACATTGAGTCCTG
CCAAACCTCAAGGAAATCAGCATACAGTAACCCCCATCAGTGTGACTGTCTACCGTTG
GATGAACATGAACAAAACCAACATTGATTGAGGCCAGATTCACTGTTGGCTGGACC
CACCTGAATTCAAGGGCAGAAATGTTGGCAAGTGGCATTTCAGGGACATGGAATATTGT
CTCCCTCTTATAGCTCTGGAGCTTCTCTTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCCCTTCACTGTAGAGCTACTGCGAACACAGCCTGAATCTACTGGATAACACCTTGT
GTCAAAACCTCTGCTTAATACCTTGACAGACAAGTTCTATGTCATTGAGGGACACTA
GATATAAATGGCTAACTCCAAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTATGATCAAAGTGGATGGATCTTCCAAAGATAACATG
GCTCTTGAATTAAAATAAGAGATATTCAAGGCAATTCTAGTTGGTGTCTGGAAAGCA
AGTTCTAAAATCTCAAATCTGTTAAATGGACAGCCTTGTCAAGACTGAAAATCTCA
TGCTGCGCAAGTGTCTGCAATACCATCTGATGTCAAGGTTATAATCTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAACAGAAA
TGTGAAATGTCAACCAACCAAGGTTGCAACCTGTCAAAAGAGTGTGAAAAGATAATAC
CACAAACACTATGGCTGCTGGAGGCCCTCTGGGGATTATGGGTGTGATATGCTTATCA
GCTGCCTCTCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCTCTCTGTATAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAGTAAAAGCAACTGTATAGGTTACCAACAAATATGTCC
AAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAIKEYSTDFPVNLTLGDLQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELNSNLQELYINHHNLLSTISPAGAFIGLHNLLRLHLNSNRQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTIEPDNALVGLENLESISFYDNRL
IKVPHVALQKVVNLLKFLDLNKNPINKRIRRGDFSNMLHLKELGINNNPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRFLPKLESMLNSNALSA LYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPFEFGQNVQRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRAATEPQPEIYIWITPSGQKLLPNTLTDKFVYHSEGTLIDINGVTPKEGGGLYTC
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSKASSKILKSSVKWTAVF
KTENSHAAQSARIPSDVKVYNLTHLNPESTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQE
YEKNNTTITLACLGLLGIIGVICLISPEMNCDDGHSHYVRNYLQKPTFALGELYPLIN
LWEAGKEKSTSLKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCGGGACTGGCGAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGTTAACCGTTCCCTCTCCATGTGTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGTTTCATTCTGCCAGTATGTGTCCTAACGGGCTGTTGTTCTCCTCGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTAACGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGCCAAAATGCCATTGAGTTATCGATGAGCAT
GCCCTCAAAGGAGTAGCTGAAACCTTGCAAGACTCTGGACTTGTCCGACAATGGATTCAAAG
TGTGCACAAAATGCCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGCCCTCAATCATGAGACAGCCCAC
AACGTGATCTGAAACGTCGGTGGATGAAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTTCACTATGGTATCTCATATGTGGTATATTGTGAGGCCAAAATCAGGAG
GATGCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCCAGAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATGTGTCCAAACTGACTGTCAATTGAGAAAAGAAA
GTAGTTGCGATTGCACTGAGAAATAAGTGGTTACTTCTCCATCCATTGTAACACATTGAA
ACTTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACCTTTAACAAACACTACAAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGTCACTGCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDQNQITSIPNEIFKDLHQQLRVLNLSKNGIEFIDEHAFKGVAE TLQTLSDLSDNR
IQSVHKNAFNNLKRARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220



N-glycosylation site.

amino acids 47-51, 94-98



cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203



Casein kinase II phosphorylation site.

amino acids 162-166, 175-179



N-myristoylation site.

amino acids 37-43, 45-51, 110-116



FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCAGCCTGGAGATGCAAGGTGAGCAAGAGGATGCTGGCGGG
GGCTGAGGAGCATGCCAGCCCCCTCTGGCTCTGGCAGCCCATCTCTCTGCTGGTGCT
GGCTCAGTGTCTGGCTCGGGCAGGGCTGCCCCCCGGCTGGAGCTGGCTCCGGCCAGG
ACCGCGCTGTGCTGCCACCGAAGGTGTTTGCGAGCTCCCCAGGGCATCCCCACCGAG
ACCGCCGCTGTGGACTTAGGCAAGAACCGCATAAACGCTCAACCAAGGACGAGTTCGCCAG
CTTCCCGCACTGGAGGAGCTGGAGCTAACGGAGAACATCGTGAAGCCGCTGGAGGCCGG
CTTCACAACACTCTTCAACCTCCGGACGCTGGTCTCGCAGCAACCCGCTGAAGCTCATC
CCGCTAGGGCTTCACTGGCCTCGAACCTGAGCAACGGAGGACATCAGGGAAACAAGAT
CGTTATCTTACTGGACTACATGTTCAAGGACCTGTACAACACTCAAGTCACTGGAGGTTGGC
ACAATGACCTCGTACATCTCACCGCCCTAGCGGCCCTAACAGCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTTCAATCCCCACGGCGCTGCTTCCACCTGCAAGGGCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCGGGACTACTCTTCAAGAGG
TGTACCGACTCAAGGCTTGGAGATCTCCACTGGCCCTACTTGAACACCATGACACCCAAAC
TGCTCTAGGGCTCAACCTGACGCTCCCTGTCATCACACACTGCAATCTGACCGCTGTGC
CTACCTGGCGTCCGCCACCTAGTCTATCTGGCTTCTCAACACTCTTCAACACCCATCA
GCACCATTTGAGGGCTTCCATGTTGATGAGCTGCTCCGGCTGAGGGATCCAGCTGGTGGG
GGGCACTGGCCCTGGTGGAGCCCTATGGCTTCCGGCCCTAACTACCTCTGGCGCTGCTCAA
TGTCTTGGCAACAGCTGACACACTGGAGGAATCAGTCTTCACTGGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCTGGCAGACTGTGGCTCTTGGTGGTCTTGG
CGCCGCTGGCGCTCAACTTCAACCCGAGCAGGCCACGGTGCGCCACGCCAGTTGTCCA
GGGCAAGGGTCAAGGACTTCTGGTGTACTGCCAACTACTTCACTCTGGCCGGCG
CCCGCATCAGGGCAACGGCCAGCAGGGTGTGGTGTGGAGGCCACAGGGTCAAGGTT
GTGTGCCGGCCGATGGCACCCGCCGCCATCTCTGGCTCTACCCCGAAAGCACCT
GGTCTCAGGCAACAGGCAATGGCGCTCACAGTCTTCCCTGATGGCACGGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTCAGTGTGCACTGGGCCAACGCCGGCGAACGAC
TCCATGCCGCCACCTGATGTGCGCACTACTGCCAGTGGCCCATCAGGCCAACAA
GACCTTCTGGCTTACATCTCAACCAAGCGGGCGAGGGAGAGGCCAACAGCACCGGCCACTG
TGGCTCTGGCTTCTGGACATCAAGACCTCATCTGGCAGGCCACCCATGGGCTCATCTTCT
CTGGGCGTCTGCTCTTCTGGCTGGTGTCTGTTCTGGAGCCGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGTATGTCGGCCGAAGTGGCACGGCATCAGCTGGCG
ACGGCGCCCGAACGTTCAACATGAAGATGATATGAGGGCGGGGGGGCAGGGACCCCCG
GGCGCGGGCAAGGGGAAGGGGCTGGTGCACCTGCTCACTCTCAGTCTTCCACCTC
CTTCCATCCCTTACACAGCTTCTTCTCCCTCCGCCCTGGCTTCTGGTCTGGCG
CCAGGCGCTCACACACTGCCCTCTTCACTGGACCTGCAAGGCCAGACCTGGGACCCA
CCTACACAGGGCATGAGCAGACTGGAGTTGAAGGGCAACCGCACGCGGCAAGTCA
ATAATTCAATAAAAAGTGTAGAATCTTCTGTGAACCTTGGTTCAATAATTATGAGTTT
TATGAAAATGTGAAATAATAAAAAGGAAAAAAACTAAAAAAAAGGAAAAAA

FIGURE 30

MQVSKRMLLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNLDLVYISHRA
FSGLNSLSQLTLEKCNLTSIPTEALSHLHGLIVRLRHLINNAIRDYSFKRLYRLKVLIEISH
WFYLDTMTPNCLYGLNLTSIPTEALSHLHGLIVRLRHLVYLRFLNLSYNPISTIEGSMHL
LRLQEIQLVGGQLAVVEPYAFRGLNLYLRVLNVSGNQLTLEESVFHSVGNLETLILDSENPLA
CDCRLLNVFRRWRRLNFNRQOPTCATPEFVQGKEFKDFDVLNPYFTCRRARIRDRKAQQV
FVDEGHHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYSPDWPQPNKTFAFISNQPGEGEANSTRATVPPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACACGCGTCCGCACCTCGGCCCCGGGCTCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC
ATCGTAGTCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCGGGAAAGCGCGATGGGGGGCCCAGCCCTCGCTCCCTGCTCCTGCTCCTGC
TGTTCGCTGCTGCTGGGCGCCGGCGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTCAAGTCAAAGATCA
CGAGGACTCATCCCTGCAATGGTCAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCACAGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCACAGCAGGGCAGTACACCTGCTCAATCTCACTATGCCGT
GCGAAGTCCAAGTCCCTCGTCACTGTCTAGGAATTCCACAGAAGCCATCATCACTGGTT
ATAAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCACTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTACCAAGAACCTCACGGAGAACCAACCCGAT
ACAGGAAGATCCAATGGTAAACCTTCAGTCAGCAGCTGGTACATTCCAGGTTACCC
GGGAGGATGATGGGGCAGCATCGTGTGCTGTGAACCCTGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCAATTGAAGTTTATACACACCAACTCGCAGTATTAGGCCAGACCC
TCCCCATCCTCGTGGGGCCAGAGCTGTGCTACACTGTGAGGGTGCAGGCAATCCAGTCC
CCCAAGCAGTACCTATGGGAGAAGGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGAAGCTGGCACACTGGCTGCACAGCCACAG
CAACATGGGCAGCTACAAGGCTACTACACCCCTCAATTGACCCAGTCCGGTGCCT
CCTCTCCAGCACCTACCGCCATCATCGTGGGATCGTGGCTTCATTGCTTCCCTGCTG
CTCATCATGCTCATCTCTGGCACTACTTGATCCGCACAAAGGAACCTACCTGACACA
TGAGGCAAAGGCTCCGACGATGCTCCAGACGCGGACACGGGATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTCATCTAGAGGCGCTGCCACTTCTGC
GCCCTCAGGGCCCTGTTGGGACTGCTGGGGCGTCACCAACCCGGACTTGTACAGCAA
CCGAGGGCCGCCCTCCGCTTGTCTCCCAAGCCCACCCACCCCTGTACAGAAATGCTGC
TTGGGTGCGGTTTGTACTCGGTTGGAAATGGGGAGGGAGGGAGGGGGAGGGGG
TTGCCCTCAGCCCTTCCGTGGCTTCTGCAATTGGGTTATTATTATTGTAAACATCC
CAAATCAAATCTGCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAACAA
AACAAAAAAACA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLQVTPHLSISISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFFFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGCTTAGGGAGGAAGGAATCCACCCCCCACCCCCCAACCCCTTTCTTCTCTTTCTGG
CTCGGACATGGACACTAAATGAACCTGAATTGTCTGTGGCAGCAGGATGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAATGCTGTTGATTCTGTT
GCTGGAGACGCTCTTTGCTGGAAACGTTACAGGGGACGTTGAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACAGCTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGAGCGTTCACTGCCCGACTTCCAGTTTACCATTTATCTGCATGCCAATTC
CCTCACTCGACTTTCCCTAATGAGTTCGCTAACCTTTATAATGCGTTAGTTGACATGG
AAAACAATGGCTTGCAATGAACTTCGGGGCTTTCTGGGCTGAGCTGTTGAAAAGG
CTGACATCACAAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGCTGACGA
TCTGGAATATCTCAGGCTGATTTAATTTAACAGATATAGACCCGGGGCTTCAGG
ACTTGAAACAGCTGAGGTGCTATTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTGCCCCATCACCCACTCGACCTCCGGGTAACAGGGCTGACCTG
CTATGAGGGTCTGGAGCAATCCCTGTTATTGCGAGATCTGCTAGAGGATAACCCCT
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGTGCTTGTGAAACCGAGTGGATCTAGCTCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTGTGAAACCGAGTGGATCTAGCTCAGGGCCTGG
CCAAGAAGAGACCTTGTGCTTGTGACCCCTGCCAACACTCTTCAAGACAATGGCAAGAG
GATCATGCCAACCCAGGGCTGCTCCAAACCGAGGTAACAGATCCAGGCAACTGGCAGAT
CAAATACAGACCCAGCAGGATAGCGACGGGTAGCTCAGGAAACAACCCCTAGCTAAC
GTTTACCTGCCCCGGGCTGAGCTGCGCACATCCAGGGTGGTTAAAGATGAAAC
TGCAACACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAGCTCTAACGTGAGGA
GCTTTCTCACAGATAACAGATCCACGATCGCAATTGTGATTAAAGA
ACCTCATCTGTGGATCTGGCAACATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATCATGGATAGCAATTACCTGGACACCGCTGCCCCGA
GAAATTCTGGGGGCTGCAAACCTAGAGTACCTGCAACCTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCATTTCAATGCGCATGCCAACACTGAGGATCTCATTCTCAACAAACCTG
CTGAGGTCCTGCTGTGAGCTGTCGGCTGGGTCTGCTCTCTAAACTCAGGCTGCAACAA
CAATTACTTCAGTACCTCCGGTGGCAGGGTGTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCAGGAAACCCCTGGAGTGTCTCTGCACAAATTGTGCTTCAAGCAGTGGCA
GAACCTCTGGGGCTCGAAGTGTGATGAGCAGCTCAAGTGTGAGACGGGGTGAACCTT
TAGAAGGATTTCATGCTCTCTCAATGACAGAGATCTGCCCTCAGCTGCTACGCTAGGATCT
CGCCACGTTAACCTGGCACAGTAAACGACTGGGTGGGGAGACCGGGACGCACTCC
AACTCTCATGACACAGCAGGGGTGTCATCTGGCTGGTCTGGGACTGCTGCTGGT
GTTGTACCTCCGCTTACCGTGGGGCATCTCGTTTATCTGAGGAACCGAAAGC
GGTCAAGAGACGAGATGCCAACCTCCCGCGCTGGAGATTAATTCCCTACAGACGCTGT
GACTCTCTACTGGCACATGGGCCCTAACACGAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTGACATTAAGACCGACGGCAACCCCAATAGGGGAGGGCAGAGGG
ATACATCTTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCGC
CCATCAGGCCGATGGCATAAGTAGATAAAATGAGCTCGCACAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCTGAAACAAAGAGCAGACACTGTGGAGAGCTGGGAGACG
GCCAGCTGCTTGTGAGAGGCCCTTGTGAGAGGCCAGCACACCCCTGCTGGAG
AACTGACAGTGCCTCGCCCTGGCCCTGGCCCTGGGGCTGTGGGGTGGATGCCGGTTCTATAC
ATATACATATATCCACATCTATAGAGAGATAGATATCTATTTCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTGGCTACCGAGGGATGGCAGTTGACAGGAAGGCATGAATGTAT
TGTAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTA
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKLLEVLLNDNLISTLPANVQYVPI
TRLRGNRLKTLTPYBEVLEQIPGIAEILLEDNPWDCTCDLSSLKEWL
ENIPKNALIGRVVCEAPTRLQGKDLNETTEQDQLCPLKNRVDSLPA
PAPPQETTFAPGPLPTFKTNGQEDHATPGSAPNGGK
TIPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCS
CDH1PGSGLKMNCNNRNVSSLADLKPK
KLSNVQELFLRDNKIHSIRKSHFVDYKNL
LDDLGNNNIAVENNTFKNLLDLRWL
YMDSNYLTDL
SREKPFAGLQNLEYLNVEYNAIQ
LPGTFNAMPKLR
LILNNNNLRLS
LPV
DVFAGVSL
SKLSLHN
NYF
M
Y
L
F
V
A
G
V
L
D
Q
L
T
S
I
I
Q
D
I
L
H
G
N
P
W
E
C
S
C
T
I
V
P
F
K
Q
W
A
E
R
L
G
S
E
V
L
M
S
D
L
K
C
E
T
P
V
N
F
F
R
K
D
F
M
L
L
S
N
D
E
I
C
P
Q
L
Y
A
R
I
S
P
I
L
T
S
H
S
K
N
S
T
G
L
A
B
T
G
T
H
S
N
S
Y
L
D
T
S
R
V
S
I
S
V
L
V
P
G
L
L
L
V
F
V
T
S
A
F
T
V
V
G
M
L
V
I
L
R
N
R
K
R
S
K
R
D
A
N
S
A
S
E
I
N
S
L
Q
T
V
C
D
S
S
Y
W
H
N
G
P
Y
N
A
D
G
A
H
R
V
Y
D
C
G
S
H
S
L
S
D

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTGATCCGGCGCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACGGGCTCGCAGCGCTCGCACACATTCTCTGCGGCTAAGGGAAACTGTTGC
CGCTGGGCCCCGGGGGGATTCTTGGCAGTTGGGGGTCGTCGGAGCGAGGGCGGAGGG
AAGGGAGGGGGAAACGGGGTGGGGAGGCCAGCTGTAGAGGGCGGTGACCGGCTCCAGACAC
AGCTCTCGCTCTCGAGCGGGACAGATCCAAGTGGGAGCAGCTCTGCGTGCAGGGCTCAG
AGAATGAGGCGGCCGTTGCCCTGTGCCCTCTGCCAGCGCTCTGGCCGGGGCGGGGG
CGGCGAACACCCACTGCCGAGCGTGTGCTCGGCCCTCGGGGCTGCTACAGCTGC
ACCACGCTACCATGAAGCGGAGCGGGAGGCCAGCTGCACTCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGGGGCGGGAGCTCGGCCCTGCTCGCCTCTGCCGGCAGGCCAGG
GCCCGAGGGGGCTCAAAGACTGTGTTCTGGGTCGACTGGAGCGCAGGCAGTCCACT
GCCAGCTGGAGCTTCTGGGGGTTCTCTGCGTGTCTCCGACCCGGCGTCTC
GAAAGCGAACACGCTGCACTGGGGAGGCCAACGCTCTGCAACCCGGCGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTGCAGGCCGAGCTGAGAGATGCGATGCCACCTGC
GCCAACCGGCTACCTGTCAAGTACCAAGTGTGAGGTCTGTGTCCTGCCCGCCCCGG
GCCGCCCTAACCTGAGCTATCGCGGCCCTTCACTGCCAGCTGACAGCGCCCTCTGGATCTCAG
TCCACCTGGGACCGAGGTGAGTGCCTGCCGGGAGCTCCGATCTCAGTTACTTGCA
TCGCCGAGCGAAATCGGCGCTCGCTGGGACAAACTCTCGGGCATGTGTTGTGTCCTCGCC
GGGAGGTACCTCGCTGGGAAATGCGCAAGGCTCCAACTGCGCTAGACGACTTGGGAGG
CTTTCGCTCGGAATGTCAGCGGCTTCACTGCCAGGCTGGGGAGGACGCCGCTTGTGACCA
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCCAGGCCCGCCGCCCCACT
GCAACAGCCCCGTGCCGAGAGAACATGCCAATCAGGTCGACGAGAACGCTGGGAGAGAC
ACCACTTCTCCTGAAAGAACAAATTCACTGAAACTCTTGAGATTCTCGATGATGGGAT
CACAGAGCACGATGTCACCTCTCAATTGCTTCAAGGGCAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGAATTCAAGTTAATTCTACGACTTCTCTGCCACTCTCAGGCTT
CGACTCTCCTGCCGTGCTTCATATTGTGAGCACAGCAGTACTGAGTTGTGATCT
TGACCATGACAGACTCTGGGGCTTGTCAAGCTCTGCTTCAAGAAAGCCCTCTCCAGCCA
AGGAAGGGAGTCTATGGCCGCCGGGCTGGAGAGTGTACCTTGAGCCCCCTGCTTGGCTC
CACTTGACACATTGCAAAACAAATGGGTGAAAGTCGGGACTGTGATCTGGGAGAG
CAGAGGGTGCCTGCTGGGGAGTCCCCTTGGCTCTAGTGATGCATAGGAAACAGGGG
CATGGGCACTCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCAGAACACTCCACACTCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
GAGCTAAATCAGAACACTCCACACTCTCCCTGATGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTACTCGGGGAGCGGTAGTGTGGGGAGAGATTTCTTATGTTTATTGGAGAA
TTTGGAGAAGTGAACATTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGAAAGGAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTCGAATCCAGGGAAAAAAATAAAAATTAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWP GP GGGGEHPTADRGCSASGACYS LHATM KRQAAE EACIL RGGALS
TVRAGAELRAV LALLRAGPGPGGSK DLLFWVALE RRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPR PG
ASNLSYRAPFQLHSALDFSSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGPFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQD NSVSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSAVV FIFVSTAVVVLVILMTVLGLV KLCF HESPSSQPR
KESMGPPGLES DPEPA ALGSSA HCTNNGV KVGDCLLRDRAEGALLA EPLGSSDA

Signal sequence:

amino acids 1-16

 **Transmembrane domain:**

amino acids 399-418

 **N-glycosylation site.**

amino acids 189-193, 381-385

 **Glycosaminoglycan attachment site.**

amino acids 289-293

 **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157, 185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469, 477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNDLCRYDFDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFKEFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLLEGN
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGCTTCTT
CCTTCTCCGTGGCTACGAGGGTCCCCAGCCTGGGTAAGA**ATGG**CCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTCTCTGGGCCTCAGCCTTCTCCTCAACCTCCAGGACCTATCTGG
CTCCAGCCTCTCCACCTCCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTCATACTCG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAAACATCCGGACAACCTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAAATTGTCCAATACAAAGACAGTGAACCGCCCTG
GTAGAGGTGCTGGAGGGTGTGCAAGCAGACTTCGAGTGCACCGCCTGCTGGAGCT
GAGTGAAGGAGCTGGTGGAGAGCTGGTGGTTTACAAGCAGCAGGAGGCCGGACCTTCTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC
CTTCCCTGTCTGGGGAACAGAGGCCCCGCGGTGGCTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAACCGGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCACTCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCAGACTGTGCCAAG
GCCTGCCTAGGTGCACTGGGGCAGGGCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCGGGAGAGA
ACAAGCAGTGAACACCGAGGGCGGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCA
CGCTGGCTGCTAAGGGCAGTTGGTGTGCTGCCATCTTCTATGGGGCTGTGGCGGGCATG
ACTGGCTACTGGTTGTCAAGAGCGCAGTGACCGTGTGCTGGAGGGCTCATCAAGGGCAGA**TA**
ATCGCGGCCACCCACCTGTAGGACCTCCTCCACCCACGCTGCCAGAGCTGGGCTGCC
TCTCGCTGGACACTCAGGACAGCTTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCCGGCAGACAAGGCCCTGGGTAAGAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGGACTGGCAGGCTCAAAATGTGTGA
ATTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTCTTAGGATTAGGTG
GTCTCACAGGGGTGGGCCATCACAGCTCCCTCTGCCAGCTGCATGCTGCCAGTTCTGT
TCTGTGTTACCAACATCCCCAACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEENILSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKGQEAAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCGTERPCGGYQCEGEGTRGGSGHCDQAGYGGEACGQCGLGYFEAERNASHLVC SACFGPCARCSCGPEESNCLQCKGWALHHLKCVDIDE CGTEGANGCAGQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFGIIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179, 177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289, 326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

Figure 41 displays a sequence of DNA or RNA nucleotides. The sequence is as follows:

TGAGACCCCTCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCCTTGCTCCAGGGCA
GCACCATGCAAGCCCTGTGGCTCTGCCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCTGGCAGCCTGCTGCCAGCTGAGCTAAAGAGGT
GCCCACCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCACGGGACCGCTCCCGGGAAAGAGGTTAGCCAGAGC
TTCGAGAGGTGGCCGGCAGGTTCTGGCCTGGAGGCCAGCACACACCTGCTGGTGGCG
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTGAGGCCGTCGGCTCTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCCGCTGTCCCCGCCAGGCCGGGCC
CGGGTACCGTCAAGGTGGCTGCCGCTGCCGACGACGGCTCCACCGCACCTCCATCGA
CTCCAGGCTGGTGTCCGCCAGAGAGCGCTGGAAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGCAGCCGCTGCTCACAGGTGTCGGTCAAGAGG
GAGCATCTGGGCCGCTGGCGCCGGCCACAAGCTGGTCCGCTTGCCTCGCAGGGGC
GCCAGCCGGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG
CTCAGGGCAGCTGTGACCTGAAAGCACCAATGACCGAGGGCACCCGCTGTCGCCAGGAG
ATGTACATTGACCTGCAAGGGATGAAGTGGCCGAGAACCTGGGTGCTGGAGCCCCGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGCCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTCTGGGCCCTGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGAGGACAGGACCAAGGCCAGGTGGTCAAGGCCAACATGAGGGTGCAGAA
GTGCAAGCTGTGCCCTGGATGGTGCCTCGTGCAGGCCAGGAGGCTCCAGCCA**TAGGCCCTAGTG**
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGAGGGTACCAAGGAGAGCTG
GGCATGACTGAAGTGTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTACCTCACCTAATTTGCTCTCAGGAATGAGAATTTGGCCACTGGA
GAGCCCTGCTCAGTTCTCTATTCTTATTCACTGCACTATATTCAAGCACTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCCCTGAC
TGGATCTGGCTAAAGTCCCTCACCACACTGGAACCTAAGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCATCCAGATAAAAGACTTGTAAAACATGAATAAACACATTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSSLRLQLQLKEVPTILDADMELVIPHVRQAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLLPPNSELVQAVLRLFQEP
VPKAALHRHGRLLSPRSARARVTVEWLVRVRDGSNRTSLIDSRLVSVHESGWKAFCVDTEAVNF
WQQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPEQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVS LPNMRVQKSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGCTGTTGTCAGTGGCCTGATCCGGATGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTCCTTCAATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGAGTGTACAGTCACCTCTTGAACTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGCTACTCGGGCTTTCTCTCCCCGTGAGTGGAAAGTTGACCA
AGGAGACACCACCAGACTCGTTGCTATAAAACAAGATCACAGCTCTATGAGGACCGGG
TGACCTTCTGCAACTGGTATCACCTTCAGTCGTGACACGGGAAGACACTGGGACATAC
ACTTGATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCTCCCATCCAAGCCTACAGTTAACATCCCTCCTGCCACCATGGGACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATACACCTGGTCAAAGAT
GGGATAGTGATGCCATCGAACATCCAAAAGCACCGTGCCCTCAGCAACTCTCCATGCTT
GAATCCCACAACAGGAGAGCTGGTCTTGTACCCCTGTCAGCCTCTGATACTGGAGAAATACA
GCTGTGAGGCACCGGAATGGGTATGGGACACCCATGACTTCAAATGCTGCGCATGGAAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCGTCTTGTAACCCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCATAGCCGAGGCCACTTGACAGAACAAAGAAGGGA
CTTCGAGTAAGAGGTGATTACAGCCAGCTAGTGGCCGAAGTGAGGAGAACAAACAG
ACCTCGTCATTCCCTGGTGTAGGCCTGGCTCACCGCCTATCATGCTGATTGCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCGTAGTTTACAGGATGCCATTGCTTCC
TACACCCCCACAGGGCCCCACTTCTCGGATGTTTAATAATGTCAGCTATGCCCC
ATCCCTCCATGCCCTCCCTCCCTACCACGTGAGTGGCCTGGAACTGTTAAAGTGGTTATTCC
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCTGGGTATGCCATTGACTCC
TTCTAAGTAGACAGCAAAATGGGGGGTCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGGATCTTGAATAGGTATCTTGAGGTTGGTCTGGCTCTTCTTGACTGAC
GACCAGGGCCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAATGGTTGG
TGATGACACTGGGGCTTCCATCTGGGCCACTCTCTCTGCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGCTCTGAATACAAGCTGACTGACATTGACTGTCCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAG
GATTTTAAACCGCTCTAAAGAAAAGAAAATGGAGGCTGGGCGCAGTGGCTCACGCC
TAATCCCAGGGCTGAGGCAGGGGATCACCTGAGGTCGGGAGTTGGGATCAGCCTGACCA
ACATGGGAGAACCCACTGGAAATACAAAGTAGGCCAGGCATGGTGTGATGCCCTGAGTC
CCAGGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGEELVFDPLSASDTGEYSCEARNNGTGPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSKKVIVSQPSARSEGEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CGCGCGTGGCCGGCGCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGAGGTTGGA
CGTGGGAACAGGGCTCTGGGCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGGCCCAGCTAG
GCTCGTCCCCACCCACCAAGTCCAGTGCGCACCGATGCTTATGCGTGCCCCCTACCTGG
CGCTGCGACAGGGACTTGGACTGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCAACCGCCCCCTGGCTCCCTGCCACCGGCGTCA
GTGACTGCTGGGGAACTGACAAGAAACTGCGCAACTGAGCCGCTGGCTGCCCTAGCA
GGCGAGCTCGTTGACGCTGAGCGATGACTGCATTCCACTCACGTGGCGTGCAGGGCA
CCCAGACTGTCCGACTCCAGCGACGAGCTGGCTGTGAAACCAATGAGATCTCCCGAAG
GGGATGCCACAACCATTGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTGGGAATGCCACATCTC
CTCTGCGGGAGACCGACTGGAAGGCCAACCTGCCTATGGGTTATTGAGCTGCTGCGGTGC
TCAGTGCAAGCCCTGGTACCGCCACCCCTCCCTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAC
CTCGCTGCCCTGAGGACAAGCACITGCCACCCGTCACTCAGCCCTGGCGTAGCCGACA
GGAGGGAGAGCAGTGATGCGGATGGTACCGGGCACACCGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCTGCAGAAGTGGCCCTGGAGATTGAGGGTCC
TGGACACTCCCTATGGAGATCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACGTAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGCTGAGGGTGGCGATTAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPGLPCPCTGVSDCSGGTDKKL
RNCsRLAACLAGELRCTLSSDCIPLTWRCGDHPDCPDSSDELGCGTNEILPEGDATTMGPV
LESVTSLRNATTMGPVTLIESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCCACGCGTCCGGTCTCGCTCGCTCGCCAGCGGGCGGAGCAGAGGTGCGCAGACAGATGCGG
GTTAGACTGGCGGGGGGGAGGAGGGCGGAGGGAGGGAAAGGAAGGACTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGGATGAAGATGTATCATGGAATGAACCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCACAGCACAGCACACCTCACTCCCCAGAGACTCTTG
GCCGTGATCTGTGGTTTCAAGCTGGCGTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCCGCATTCCCGAGAATGGCTTCAGGACCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCCATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCTGAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTTCTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCTTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCGGGATTAAACTT
GATGGGTCTGCTATCTTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCCAAGTGTGACTACCTCAATGGTAGTCACTGGAGATTCTGTCT
GCCACCCGGGCTTGTGAGCGCTACAAACACGGAACTGTGGTGGAGTTTACTGCGATCTC
GGCTCAGCCTCACAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAACGTGGCCCAAGCACCCTAGAGACCTCTCTGA
CCACGTGGAGATTGTGGCTTCACGGCAACCAGTGTGCTGTGCTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTCAAGGCCACTTCCCCCAAGGGGCTCCCGGAG
TTCCAGCAGTGACCTGACTTGTGGTAGACGGCGTGCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGTGAGTGCCTTAGGCCCCGGTACATGGCCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAAGGCCAGCATACCCGGCTCAGGGGACACGG
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGCTCAGGCTTCTGAGCTGCTCCAA
GTCTGTATTCACTCCAGGTGCCAAGAGAGCACCCACCTGCTGGACAACCCGTACATA
ATTGCCAGCAGCGAGAGGGAGTGGCATCCACCAGCCAGGCATCCATGCCCCACTGGGT
GTTGTCTTAAGAAACTGTATTGATTAATTTCCAAAGTGTCTGAGTGTCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCTCTCTTGTGTTAGACAAATGTAACAA
AGCTCTGATCTTAAATGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTCTTGACACAGACTGATTAATTTAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKAGTKRLCLKHFNGLGWI PSDNSICVQEDCRI
PQIEDAEIHNTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPI CQGCLRPLAS
SNGYVNISELQTSFPVGTIVSYRCFPGFKLDSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSYKITYTCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACACGCGTCCGCTCCGCGCCCTCCCCCCCCTCCCGTGCAGGTCGGCTCGGTGGCTAGAGA
TGCCTGCGCGGGTGCAGTTGTCGCGCACGCCCTGCCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGACCCGAGTCGGGCCATGAGGCGGGAAACCGCGTACAGG
CCGTGCTGCGTGGCGTGCCTGGGTGGGCTGCGGGCGACGGGTCGCCCTGCTGAGTGC
TCGGATTGGACCTCAGAGGGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCATGATACTTCTCGAAGACTGAACATTGAGGAAGGCAAAGAACCT
GCAGGAGGGATGGAGGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAAATGATAGAA
AAGTTATTGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
ACAATTAGGAACCTGGTATGGATGAGCGTCCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCACTGGAATGATGA
CCGGTCAACATGAAGAACATTCTATTGCAAATATTCTGATGAGAACCCAGCAGTCCCT
CTAGAGAAGCTGAAGGTGAGGAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCTCTCCCTCTTGCTGTCACACAGTTGTATGTTGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTACCAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGAGACCCGGCAGACCTGAAGAATATTCTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGCTTGTACTATGACAACATGGCTGAAACCATCA
GAAAGTGGTTGTGACTCTGGTAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCAAGACCAAATGGGAGAGTAAGGAGTCTGGATGGTGGAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACATGGAAAAGAAATGATAAGCAAATC
CTCTTATTCTATAAGGAAAATACAGAACGGTCTATGAAACAGCTTAGATCAGGTCCTGT
GGATGAGCATGTTGCTCCACGACCTCTGGTAGGCCACGTTGGCTGTATCCTTAT
CCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCATTGGTTGGTGTATCTAACTTTAAGGGACAGAGCTTACCTG
GCAGTGTAAAGATGGGCTGGAGCTGGAAAACACCTCTGTTCTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETEITTPVLPEETQEEDAEEKTFKESREAALNLAYILIPSIPLLLLLV
VTTVVVCWVWICRKRKREQPDSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGGGACTTGGGGCGCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT
GTTGCCTCCTGCAGCCTAACCCGGAGGGCAGCGAGGGCCTACCACCAATGATCACTGGTGT
GTCAGCATGCCTTGTGGACCCCAGTGGCGTCCCTGACCTCGTGGCTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCAGCTGCAGGAGGCCGATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCTGTTGACACGGGGCTGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCAACCAACCTCAACCCACAGGGAGGTCTTATTGTTCCACTAACATTTCGGAACTCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTAGAAGTCTTGATCCAACTACCAAAGCTGCTGGAGCTGA
GGCAGAGAACAGAGGCCGGAGGAGCAGACTGCCCTTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCCT
GGACAACGTGGCTGCCGAGCAGGCACACAAACCTCCAAAGTGGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGATACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTAAAGACCCCTGGGATTTGACCACAAATGGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCAAGGGAGGAGCAGGTGCCGAGGGTGCCTGATGGCTCTGCCGCTGGACATGT
TCTTGATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRQRQTAISLQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAEEQAHNLPLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LDMLFLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCTCTTAAACATACTTGAGCTAAACTAAATATTGCTCTGGGGACCTCCTTAGCCT
TAAATTTCAGCTCATCACCTCACCTGCCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCCACAGACCTGGATTCTCTAGCGCTCCATCTGGAGTGGGCTGGGGGGCCT
CCACCGCTGTGAAGGGGGGGTGAGGGTGAACAGAAAGGCCAGTGGGGCACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCCCGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTGTATGAGGCCACAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTTGTTACATGATGAAGATGCTGGGGCATGTTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGA
GCACCCAGAACCACTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCGCAAAAGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGTCAGGACGAGAACGCAACCCCTCA
GGATTGCCCTCTGGGCTTGGGGAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGGAGAGAACACCTGCTCTGGGCACTG
GAGGTGTGCAAGGGCGTATGGGCTCTGTGATGACAACCTGGGAGAAAAGGAGGA
CCAGGGTGTATGCAAGCAACTGGGCTGGGAAGTCCCTCTCCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGGTTGGCGCATGGCTGGATAATGTTGTTGCTCAGGGAGGAG
CAGTCCCCTGGAGCACTGGCAGCACAGATTTGGGGTTTACGACTGCACCCACAGGAAGA
TGTGGCTGTCATCTGTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCATGACTGCATGGGATGAAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCTGATTCTCAGGCCCTCAGAGTTGG
ATCAGAAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGGAACTACATCA
CCACCTTCCATGTCACATTGACACAGCAGATCCCGCCTCCATAATTGTTGAT
CAACTACTTAAACATTCATA
CACCAATTGTCCTGTTCTCTGAAGAACCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATAAAATTCTGGTAACCTTATTACAATAAAAGATAGCAC
TATGTTCAAA

FIGURE 54

MALLFLSLILAICTRPGLASPVGRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCAGASGTPSGILYEPPAEEKQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPQHCKGRVEVKHQNQWYTCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCGGCGACCGCGGGCGACCGCTGGCCGGTACCCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCGGG
CGTCTCGGCTCTCCGGCTGCTGCAGTGGGTGCGCGGAAGGCCAACCTGCCGAATGCTG
TGGTGGTATCACAGCGCCACCTCAGGGCTGGCAAAGAATGTGCAAAGTCTTCTATGCT
GCGGGTCTAACTGGTGCTGTGGCCGAATGGTGGGCCCTAGAAAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGCACCTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC
GACATACTTGTCACAAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGG
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCCTTTCGATCAGCATATGCAGCCTCAAGCACGCAACCCAGGTTCTTGA
CTGTCTCGTGGCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGTACA
TCCACACCAACCTCTGTAAATGCCATCAGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCCTCCTGGCTGTTTATCTCGAA
CTCTGGCTCCTGGCTCTCTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACGAGCACTTTAGGTTGC
TTACTCTACAAGGGACAGTGATTTGAGACTTTAATGGAGATTGCTCACAAGTGG
AAAGACTGAAGAAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCAGGGTGAGGGAAACACTTAAGGAATAAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTAAACAGTAAAAAAAAAAGGGCGCCCGGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPPLLFGCLGVFGFLRLLQWVRGKAYLRNAVVTITGATSGLGKECAKVFYAAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEBILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAAYASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTPVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDFLFTQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMFIFPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACACGCGTCCCGCGACCGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC
AGGGAGGAGCACCGACTCGCGCACCCTGAGAGAGATGGTTGGTGCCTATGTGGAAAGGTGATTG
TTTCGCTGGCTGTGATGCCGCTGGCCCTGTGATGGGCTGTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTCGTCACCCCTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGAGTCGCCCCCTTCAGGACTGAACATGA
AGAGTTATGCGGCTTCCTCACCGTGAGATAAGACTTACACAGCAACCTCTCTCTGGTTC
TTCCCATGCTCAGATAACAGGCAAGAGATGCCCTAGTAGTTCTGGCTACAGGGTGGGCCGG
AGGGTTCATCCATGTTGGACTCTTGAGGACATGGGCTTATGTTGACAAGTAACATGA
CCTTGGTGACAGAGACTCCGGACACAGCTCCATGCTTACATTGACAACTTCA
GTGGCAGCAGGTTTACTGATGATACCCACGGATATGCACTGAGTCATGAGGACGATGT
ACGACGGGATTATACAGTGCATAATTAGTTCTCAGATAATTCTGAATAATAAAAATA
ATGACTTTTATGTCATGGGGAGCTTATGCAAGGAAATATGTCAGCAGCATTGACACCTC
ATCCATTCCCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTAGGGGCTATGCCAGAATTCTGTCACAAATTGGCT
TGTGGGATGAGAAGAAAAAAAGTACTCCAGAAGCAGTGCCTATGCAATAGACACATC
AGGAAGCAGAACTGGTTGGCCTTGAAGAATACTGGATAACTACTAGATGGCAGCTTAC
AAGTGATCTTCTTACTTCCAGAATGTTACAGGATGTAGTATTACTATAACTTTGGCT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGGTCACTCCAGAGGTGAGACAA
GCCATCCACCTGGGGAAATCAGACTTTAATGATGCAAGCTTACTAGTTGAAAAGTACTTGGAGA
AGATACAGTACAGTCACTGGCATGTTAACCTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAAGTGGACATCATGTCAGCTGCCCTGACAGAGCGCTCTGATGGC
ATGGACTGGAAAGGATCCCGAAATACAAGAAGGAGGAGAAAAAAAGTTGGAAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTACATCCGGCAAGCGGGTGACTTCCATCAGGAATTATTC
GAGGTGGAGGACATATTTCACCTATGACCAAGCTCTGAGAGCTTTGACATGATTAATCGA
TTCATTTATGAAAAGGATGGATCCCTATGTTGGAATAAACTACCTTCCAAAAGAGAAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCTGAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATGCAAGATTTCATCAATAAAATTATCTGAAACAAAGTGA
TTTGTGTTGGGGGAGATTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGAGTGTGACACTGAGACAAGATGTATAAATGA
AATTGGTCTTGAATAGGAAGTTAAATTCTCAAGGTAAGTGAAGGAGCTGAGTTG
TAACAAACAAAGCTGAAACATCTTCTGCAATAACAGAAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAAATAATGAGTGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTTAAAGTCTTGAACAAAAGAATTCTTGAATAA
AAAATATTATATAAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYI EAGKIQKGREL
SLVGPFPGLNMKSYAGFLTVNKTYNSNLFFWFPQAQIPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLDRDFPWTTILSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPVREVKINLN
GIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEA
FEI
LDKLLDGDLTSDPSYFQNV
TGCSNYYNFRLRCTEPEDQLYYVFLSLP
EV
RQAIHVG
NQTFNDGTIVEKYL
REDTVQSVKPWL
TEIMNNYKVLIYNGQLDII
VAAALTERSLMGMDWKG
SQEYKK
AEKKV
W
K
I
F
K
S
D
S
E
V
A
G
Y
I
R
Q
G
D
F
H
Q
V
I
R
G
G
G
H
I
L
P
Y
D
Q
P
L
R
A
F
D
M
I
N
R
F
I
Y
G
K
G
W
D
P
Y
V
G

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGGAAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAAACAT
TTTCCCTTCTAACAAAGTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGTTCTCTT
CTGGAGAAGAAAGGGCTGAGGGCAGACAGGGCACTCTACAGGGTACCGACTCCCTG
CTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAATAGGAAGGAATTGGTGTGCAATATCAGACTCTGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGGCTGCCAACAGCTTTCAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGGTTAGTCTTAATATCAAATTGACTGGCTGGG
TGAACCTAACAGCCTTTAACCTCTGTGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAAAATTTAAAAAAAGCAAGTATTATGACATAAGGCTAGA
GACCAAAATAGATAACAGGATCCCTGACACTCTAACAGGGAGAAAGTATGTTAAAATA
GAAAACCAAATGCGAGAGGAGACTCACAGAGCTAAACAGGATGGGACCTGGTC
AGGCCAGCCTTCTCTCCGGAAATTATTTGGTGTGACCAACTCTGGCTTGTGTTT
GCGAACATGTGAGGGGCCAACCGGGGAGGTGGAGCAGATGAGCACACAGGAGCCGCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGAGGCCCTGGCCCCGGGCTGGAGGTGG
ACAGCGCTCTGTGCTCTGTGCTAGTGTCTGGTCTGTGGCCCCCAGCAGCCGC
ATGCCCTAGTCAGCCCTTCACTCTGAGAACATGACTGGACCTTCACCAACTTGACCGT
CCCAAAGGGACGGGGCCCTCATGGGGGCGATCATAGACAGGGCAGAAGAGGACAACAA
ACTCTGACCATCAGGTGGCTCATAGACAGGGCAGAAGAGGACAACAAAGTCTGTTACCCG
CCCTCATGCGAGGGCTGAGCAGCTGGCCCTACCAACAAATGTCACAAAGCTG
CATCATGACTACTCTGAGAACGCCCTGCTGGCTGTGGAGGCTCTACAGGGGCTGCA
AGTGTGCGGGCTGGATGACCTCTTCATCTGGTGGAGCATCCACAAAGAGGAGCACTAC
CTGTCAGTGTCAAAAGACGGGACCATCTGACGGGTGATTGTGCGCTGTGAGGTGAGGA
TGGCAAGCTCTCATGGCACGGCTGGATGGGAGCAGGATTACTCTGGACCTGTCCA
GCCGGAAAGCTGCCGAGACCTCTGAGTCTCAGCCATGCTGCACTATGAGCTACACAGCGAT
CTTGTCTCTCTCATCAAGATCCCTTCAAGACACCTGGCCCTGGTCTCCACTTGT
CTTCTACATCTACGGCTTGTAGTGGGGCTTGTCTACTTCTACTGTCAGGAGCCGAGA
CCCTGAGGGTGTGGCCATCAACTCCCTGGAGACCTTCTACACCTCAGCATCGTGG
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGCCCTGCCCTGGCTGCACCGGGC
CGGGGTGGAATACGGCCCTCTGGCAGGCTGCTGGACAGGCTGGGACTCACTGGCC
AGGGCTTCATATCACCAGCAGGAGCATGACTCTTGGCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCCTCCCTATCCGGGCCATCAACT
GCAGATCAAGGAGGCCCTGCACTGCTTACAGGGCGAGGGCAACACTGGAGCTCAACTGG
TGTGGGGAGGACCTCCAGTCAGCAGGGCCCTGCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCGCCCTGGAGGCTCAACTCCAGTGAGGGCTGACCCCTGTACACCC
CAGCAGGGACCGCATGACCTCTGTGGCCCTCTACGGTAAACGGGCTACAGCGTGTTT
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTCAAGATGCTCAAATGCC
ATTCACTCTCTGACAAAGACTCCCTTGTGGAGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTCTGGGAAACAAAGGTGAATGGGGAGGTAAGAAGGGGTTAATTGGT
ACTTAGCTCTAGCTACTTCCAGCCATCAGTCATTGGTATGAAAGGAATGCAAGCGTA
TTCAATATTCCCAAACCTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLLQASLFFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSDRSVVLSSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNVNKLIIIDYSENRLLAGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVMKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPDPESSAMLDYELHSDFVSSLIKIPSDTLLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSSVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHPPDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFGTKSGKLKKVRYEFRCNSNAIHLLSKESILLEGSYWWRFNYRQLYFLGEQR

Signal sequence:
amino acids 1-32

Transmembrane domain:
amino acids 71-87

N-glycosylation site.
amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.
amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristylation site.
amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

FIGURE 64

MTTWSLRRR PART LGLLL VV LGFLV LRR LDW STLV PLR RQL GL QAK GWN FM LED ST FW
I FGG SI HY F RVP PREY WR DR LL K M KAC GL NT LTT Y VP WNL H E PERG K F D F SG N LD LEAF VL MA
A E I GL W V I L R P GP Y I C S E M D L G G L P S W L L Q D P G M R L R T T Y K G F T E A V D L Y F D H L M S R V V P L Q
Y K R G G P I I A V Q V E N E Y G S Y N K D P A Y M P Y V K K A L E D R G I V E L L L T S D N K D G L S K G I V Q G V L A T
I N L Q S T H E L Q L L T T F L F N V Q G T Q P K M V M E Y W T G W F D S W G G P H N I L D S S E V L K T V S A I V D A G S
S I N L Y M F H G G T N F G F M N G A M H F H D Y K S D V T S Y D Y D A V L T E A G D Y T A K Y M K L R D F F G S I S G I P
L P P P P D L L P K M P Y E P L T P V L Y L S L W D A L K Y L G E P I K S E K P I N M E N L P V N G G N G Q S F G Y I L Y E
T S I T S G I L S G H V H D R G Q V F V N T V S I G F L D Y K T T K I A V P L I Q G Y T V L R I L V E N R G R V N Y G E N
I D D Q R K G L I G N L Y L N D S P L K N F R I Y S L D M K K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S
S T P C D T F L K L E G W E K G V V F I N G Q N L G R Y W N I G P Q K T L Y L P G P W L S S G I N Q V I V F E E T M A G P A
L Q F T E T P H L G R N Q Y I K

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGGGAGCTGAGAGGCTCCGGCTAGCTAGGTAGGGGTGGACGGGCTCCAGGACC
CTGGTGAGGGTCTCTACTTGGCTTCCGGGGTCAAGACGCGACCTACGCCAAAGG
GAGCAAAGCCGGCTGGCCGGAGGCCCCCAGGACCTCATCTCCAAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCGGCGTCTAGACTAGAGGAGCGCTGTAAACGCCATGGCT
AAGAAGCTGTCGCTTCGCTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGCTCGTAGTGGATAGGGCATGACGGTTCTCTAGACGGGCC
CGTTCGCTATGTCGCTGGCAGCTGCACACTTTCGGGCTGGCGGGTGTGTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCAACCCCATACAGTTATGTGCCCTGGAACTA
CCACGAGGCCACAGCTGGGGTCTAACTTAACTTAACTGGCAGGGGACCTCATGGCTTCTGA
ATGAGGAGCTAGCGAACCTGGTGTCTAGACGACAGGACCTTACATCTGCAAG
TGGGAGATGGGGGCTCCCATCCTGGTGTCTGAAAACCTGAAATTCTACATAGAACCTC
AGATCCAGACTCTTGGCCAGTGGACTCTGGTTCAGGTCATGGCTGCCAAGATATTC
CATGGCTTATACAAATGGGGCAACATCATTAGCATTAGGGAGAAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTTCCGTGACTGCTAG
AGAAAAAGATCTGCTTCACACAGATGGGCCAGAAGGACTCAAGTGGCTCCCTCCGG
GACTCTATACCACTGTAGATTGGGGCATGGTACAGCAACATGACCAAATCTTACCCCTGTT
CGGAGTATGAACCCCATGGGCAATTGTTAGCTACAGCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCAGAATCACTCCAACGGCTCTGCTGAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTGGGGAGCCAGTGTGACATGTCATGGTCCATGGAGGTAACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCTGGATTACTACAGCTATGACTATGATGCA
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTTGCTTCTGAGATGTCATCAGCAAGT
TCAGGGAGTGGCTTGGGACCTTACCTTCCCGAGGCGAACAGATGATGCTTGGACCTGTG
ACTCTGCACTGGTGGGCAATTACTGCTTCTCTAGACTGCTTGGCTTGGGCCCAT
TCATTCAATCTGCAATGACCTTGAGGCTGTCAGCAGGACCATGGCTCATGTTGAC
GAACCTATGACCCATACCAATTGGGAGGCAACACATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGTCTATGTTGATGGGATGGGGTGTGGAGGCGAACATGGAG
AGACAAACTATTGGGAGCGGGAAACTGGGGTCCAAACTGGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGTCAACAGCACTGACTTCAGGGCTGTGAGGCCACAAATTCTG
GGGCAAAACATCTTCAATTAGGCTCAGGGACACATTCTATACCTCTGGGATGG
GTGGTTTCCCCTCCAGTTGCAAAATGGCCATACCTCTCAAGCTCCCTGGCCCCACATTCT
ACTCCAAACATTTCAATTAGGCTCAGGGACACATTCTATACCTGGATGG
ACCAAGGGCCAAGTGTGGATCAATGGGTTAACCTGGGCGGTACTGGACAAAGCAGGGCC
AAACAGACCCCTACGTGCAAGATTCTGCTGTGTTCTAGGGAGCCCTCAACAAATTAA
CATTGCTGAAACTAGAAGATGTCACCTCTCCAGGCCCCAAGTCACATTGGGAGGCTAC
CTCAATGACACTAGTACTTTCACAGGACACATATCAATTCTGGTGTGGCTAC
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTTGAAGGTAGGCCGGCATGGTGGCT
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCAACATGGTGAACACCCCGTCCACTAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGAGGAGGTTGCACTGAGTGGAGGTTGACCAACTGCACCCAGCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAA

FIGURE 66

MAPKKLSCRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPWLLRKPEIHLRTSDPDFLAAVDSWFVKLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPVLNSEYYTGWLWQGNHSTRSVAVTKGLEMLKLGASVNMMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMML
GPVTLHLVGHLLAFLDLCPRGPIHSILPMTFEAVKQDHGPMLYRTYMTHTIFEPPTPFWVPN
NGVHDRVAYVMVDGVFGVVERNMRDKLFLTGKLGSKLDILVENVNMRSLFGSNSSDFKGLLK
PILGQTIILTQWMMFPLKIDNLVKKWWFPLQPKWPYQPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSAITLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAAACAGCTCTGCAAGCCCCAAAGTTGAGCATCTGATGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAGCTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGCAGTTTAGTGCACATCCAGATGTCAAAAACGATTT
GCCTTCCTCTCACATGGTAGACCGATGACAGCTATATCCAGCTTTGGTGTGTT
CTTGTCAAGAAGTTAGTGAAGAATAAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTCATG
CTGTCGGGGTGGCCGATGCTGCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAATTCTGCTAAGATTCTCAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAGAAAGTTGAAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTTGCTGAAATTCTGCTGGGTGTTATTGCTCAAAA
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AACTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTTGCTCCACATCTTACAAAGTTAGTCATTCTATAATGACGGCAC
TAAACTCTGGTACTGAAACGCCCTAAGAAAATGATGAAATGTCGCTGAGCTGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTCAGCCTCTCAATTACAGGAACTGGAT
TTAAAGTCCAATAACATTGCGACAATTGAGGAATCATCAGTTCCAGCATTAAAAGCACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTTATTACCCATGTCA
AAAACCTGGAGTCACTTTATTCTCTAACACAAGCTGAAATCCTTACAGTGGCAGTATT
AGTTTACAGAAAATCAGATGCTTAGATGAGCTACAACACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCAATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCTAAAGTTGAGGACTTGAATCTGGGACAGAACTGCATCACC
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGGCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCAGGGTTGTTG
TGGAAAGATCACCTTTTGTACCCGCCACTCGAAGTCAGGACTTGAATCAAGACATA
AATATTCCCTTGCACATTGGATTAAAAACTAAGATAATATGCAAGTGTGAGAAC
AACTTCTTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCAATTAGGAGTAG
ATACATCTTTAAATAAAAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAAGGTTTAAGTCATTCAATTCCAAATCATTTTTTTCTTTGGG
AAAGGAAAGGAAAATTATAACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELPIEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMGLESRLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAAELELQNCELERIPIHAIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNVKDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMILKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI



Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

FIGURE 70

MEVLVRLMLPLTLLILSCLAEELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPESENCTWTI
ERPEPKSIRIIIFSYVQLDDGSCESENIKVFDGTSSNGPLLGQVCSKNDYVPVPESSSSTLT
FQIVTDSARIQRTVVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKOCKFDLAIYDGPSTNSGLIGQVCGRVPTFESSSSNLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSIITYNTIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYIITEDDVIIQSQNALGKYNTSMALFESNSFEKTIILESPYYVVDLNQTLFVQVSLHTSDPN
LUVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKPLRSMSSVYL
QCKVLLCDSSDHQSRCNCQCVSRSKRDISSYKWTDSIIGPIRLKDRSASGNNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GA CGGG AAGAAC CGCG TCCC GAGG CGCG GGAG GCCT GCAG AGAGGA CAG CGGG CCT GC CGCG
GGAC **ATG** CGGCC CAGG AGCT CCC CAGG CT CGCG TCC CGT GCT GTT GCT GTG CTGC
T GCG CGCC CGCC CGT GCG CTG CCA CAG CGC CAC CGC CTG CAG CCA CAG T CGG C AT CTC ACTG
CTGG AC GCG CGC CAG CTG CCG CGT GGG T GAC CAG GCA AGT T CGG C AT CTC ACTG
GGG AGT CT TCC CGT GCG CAG CT CGT GAG GTGG T CTGG GTG T ATT GG CAAA AGG AAA
AGA TAC CGA AGT AT GTG GAA AT TAT ACC CT CCA T GGG CAG AT TTTT CAGG C
TTT GGG CAC T AT TAC AG CAA AAT TTTT AAT GCG CAA CAG T GGG CAG AT TTTT CAGG C
CTC TGG T GCG CAA AAT AC ATT GT CTT A CT CCA A C AT GCA AGG CTT TAC CT TGT GGG GT
CAG AAT ATT CGT GGA AT CGG C AT GAG T GAG GGG CCA AGG AGG GAC AT TGT CAG GAA
CTT GAG GTAG CGC ATT AGG CAC GAG CTG AC T CGC TT GGG ACT GT GAC T ATT CCG TTT GT
ATGG TTT CTC CGC TCT CCG T GAGG AT GAA TCC AGT CATT CGC ATA AG CGG CAA ATT TCC AG
TTT CTA AGAC AT TCG CAG GAG CT TGT AAT GAG AAT TGT GAG A CACT TGT CAG GAG CAG TTT CAG T
TCGG AT GTG CAG CGAG GAG CAC CGG AT CAAT AGG CAA CAG CAC AGG CTT CTG GCG CTGG T
ATATA AT GAA AG CGC CAG T CCGGG CAC AGT AGT CAC CA AT GAT CGT GTGG GAG CTGG TAG C
TC TGT AAG C AT GTG CTT CTA CAC TGT CGC AGT GAT CGT TATA ACC CAG GAC AT TTTT GCG C
TCA AAT GGG GAA ACT CGC AT GCA AT AGA CAA CTG TCT GGG C TATA AGG AGG GAG CTGG
AA TCT CTG ACT TAT CTT CAA AT GTG AAG AAT TGG GTG AAG CAA CT GTG TAG AGA CAG TTT CAG T
GAG GAA AT CTTT GTG AAT AT TGG GCC CAA CACT AGAT GGC ACC AT TT CTG TAG TTTT GAG
GAG C GAG CTG GAG CAG TGG GCT CTG CCA TAA AGT CAAT GAG GAG AAG CT ATT TAT GAA AGC CTA
TAC CTG CGAT CCC CAG AAT GCA ACT GTG CAC CCG CAG AT GTG TGG TAC AC AT CCA AGC CTA AAG
AAA AAT TGT C TAT GCG AT TTT CT TAA AT GGG CCA AC T CAG GAG CAG CTG TCT GGG CCA T
CC CAA AG C TTT CT GGG GGG CAA CAG AGG GTG AAG ACT TGT GGG CCA TGG ACAG CAG CCA TTA ACT G
GAT T CTT TGG GAG CAA AT GTG CATT AT GTG TAA GGT GAC T GGC CAC AG CTA ACC AT TGT CAG AT G
CGT GT AAT GGG GCT TGG GCT TCA GGG CTT A CAA AT GTG TAC TGT CTA **AA** GTG CAG CAG AGT GGG CT
AT GCT GCA AGG TTA GTG CTA AGG CT TAG GAA ACT AT CAG GTG TGT TATA AT TGT GAG CAC AT GGG A
AAG CCA AT GTG TAA ACT TGG ATA AGA AAT ATT TGG CAG TT CAG CCCT TT CCA CTT CCA CACT A
AAT TTTT CTT AAT TAC CCA GTG TAA CATT TAA CT CCA GAG TGT GCA CTT TG CATT AAAGT C
TCT CAC AT TGT GAT TGT TCC AT GTG GACT CAG AGG TGA GAA ATT TT CAC ATT ATAG T
CAAG GAA ATT TGG GT TAT ATGG ACC GAA CTG AAA ATT TT TGT GAG AAG CCA TAT CCCC CATG
ATT TAT ATAG T TAT GTG C AT CACT AAT ATGG GAT ATT TT CTGG GAA AT GCA TTT GTG CTAG TCA AT
TTT TTTT GTG CCA AC AT CATA GAG TGT ATT TCA AAA AT CCTAG AT GCG ATAG CTT ACT A
CAC CTA AT GTG TAT GTG TAT AGC TGT GCT CCG TAGG CTA CAG A C AT A CAG C AT GTG TACT G
AA TACT GTAG CC ATAG TAA CAG TGG TATT GT TAT ATG CAA AC AT TGG GAA AC ATAG GAG GAG
GTAC AGT AAA AAT ACT GT A AAT AAT ATG TG CAC CT GT TAT AGG GACT TAC CAC AGA AT GGG AG
CTT ACAG GACT TGG AAG TT GCT TGG GTG AGT CAG T GAG TGA AT GTG AAG GCT TAGG AC ATTA
TTG A AC ACT GCG CAG AC GCT TATA AAT ACT GT TAT GCT TAGG CTA CACT AC ATT TATA AAAAAA
GTT TTT CTT CTT CA TAA TATA AAT TAA CATA AAG TGT ACT GT TACT GT AACT TT CAA AC GT TTT AATT
TT TAA AAC CTT TGG CTT GT TTT GT AATA AAC ACT TGT CTT AAA AC AT AA ACT CATT GTG CAA
AT GTAA

2021/05/20 10:55:23

FIGURE 72

MRPQEPLRLAFLPLLLLLLPLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTMDRGAGSICKHGGFYTCSDRYNPQGHLLPKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLQRQVGSWLKVNGEAIYETY
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCGGATGTCCTGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGAAGTAGTTATTGAGCATCGCTCTCATATCACAGTGGCCATC
TGAGGTGTTCCCTGGCTGAGGGTAGGCACGATGGCAGGTGCTCAGGCTGGTGTG
CTTCTCACTTCATCGGACACGAGGCTCTGGTCCAAGGCTCTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCATCGAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCCTGAGGCTGCTGGACTAAGTTGGCCGGAAG
GACCAAGTTGAAACAGCCTTGAAGAGCTAGCTTGAAACTTGAGCTATGGCTGGGTGGAGA
TGAGTTCTGGTCATCTAGGATTAGCCCAAACCCAAGGTGCTGGGAAAATGGGTGGTG
TCCCTGATTGGAGGTTCCAGTGAGCCAGACTTGAGCCTATTGTTACAACCTATCTGAT
ACTTGGACTAATCGTGATCCAGAATTATCACCAACAAAGTCCATATTCAACACTCA
AACTGCAACAAACAGAATTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTT
ACTCTAACATACCTGCCCTACTACTCTCTCTGGTCAGCTCAGCTCCACCTCTATTCCACGG
AGAAAAAAATTGATTTCATGTCAGAAGTTTATTGAAACTAGCACCATGTCTACAGAAC
TGAACCATTTGTGAAATAAAGCAGCATTCAAGAATGAAGTGCTGGTTGGAGGTGTCC
CCAGGCTCTGCTAGTGCTCTCTCTTGGTGTGAGCTGGTCTGGATTGGATTTGC
TATGTCAAAGGTATGTAAGGGCTTCCCTTACAAACAGAATCAGCAGAAGGAATATGAT
CGAACCAAGTAGTAAAGGAGGAAGGCCATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGCATGCC
GCTGAAGTTAGATGAGCAGAGAAATGAGGAGACACCCCTGAGGCTGGTTCTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAGAAAGTCCACCC
GGTCTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGACCAAAAGGAATG
CCTCTCTTATTGTAACCCCTGCTGATCCTATCCTCTACCTCAAAGCTTCCACGGC
TTCTAGCCCTGCTATGCTTAATAATCCTACTGGGAGAAAGGAGTTTGCAAAGTGC
GGACCTAAACATCTCATCAGTATCCAGTGTAAAAGGCCCTCTGGCTGTGAGGCTAG
TGGTTGAAGGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCGCAGCTCAGAC
CCTTCTCTGCTGAAAGGAGAACACGTATCCCACCTGACATGTCCTCTGAGGCCGGTA
AGAGCAAAGAATGGCAGAAAATTAGCCCCCTGAAAGGCCATGGAGATTCTCATAACTTG
ACCTAATCTGTAAAGCTAAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTGTTCTCTGAACACATTGAGTTGG
ATCATCTGTGTTAGAACACACACTTACTTTCTGGTCTCTACACTGCTGATATTCTCT
AGGAATATACATTACAGTAACAAAATAAAACTCTTAAATTCTATTATTTTATCTGA
GTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCAACATAGTGAACCTATCTGGGAAGCTATTCTCT
GTTTGATATTCTAGCTTACTTCCAAACTAATTCTATTCTGGTCTGAGACTAATCT
ATTCTATTCTCTAATATGGCAACCATTAAACCTTAATTATTAAACATACCTAAGAAG
TACATTGTTACCTCTATACCAAGCATTAAAAGTGCCATTAAACAAATGATCTA
GCCCTCTTCTCAACAAGAAGGGACTGAGAGATGCAGAAATTGTCAGAAGAAAATTAA
AGCAATTAGAAAATT

FIGURE 74

MARCFSLVLLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVVGDFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF
AAKYCYNSSDTWTNSCIPETITTKDPIFNTQTATQTTEFIVSDSTYSVSPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGATTCGGTGCGCGACTTCACGATGG
CTCGCCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCCTACTCGTGAGGAA
ACTGCGCCGCTCTGCCACGGCTGCCACCCAACCGCAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCTGTGATGATGAGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCTATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTGGATATTGCATGGGCCTACTTACATCACACTGCATAGTGTCC
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGGAGTTCTTGGCAA
TTGGTCTAATGACTGCCAATCATTGGCCCTATCTATGTCGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGGAAGGGTGGATGTTGGACGCTATCTGATGTTAGTACGGGTAC
AAAGTGACCATCACCCCTACCAAGCAACTCCTCACCTGATCTGTTCCAAGGTGGCAA
GGAGGCAATGGCGGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGGCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGGCTGTGGCTCAACCCCCACACAGTGTCA
TGCGGAAACAAAGAGATAAAATAAGATCCTCATTGGCAGTGCTTCTCTCTGTCAATT
CCAGGCTTCCATAACCCACAAGCGCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGCAAGCATGCACTGAGCTCTGATTTAAAGAGGCATCTAGGGAAATTGTCAG
GCACCCCTACAGGAAGGCTGCCATGCTGTGGCCAACGTGTTACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCAAGCTGGGTAGTGTGTTACTGCTTATC
AGCTATTGACACATCTCATGGTTCTCCATGAAACTCTGTTGTTCATCATTCTCTTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTTAACCTTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCCCAAGGACTCTGCTTCTTAAGGCCCTCTGGCTCGTTATGGTC
TTCACTAAAAGTATAAGCCTAACTTTGTCGCTAGTCTCAAGGAGAACCTTTAACCAAAAG
TTTTTATCATTGAGACAAATTGAAACAACCCCCCTATTTGTTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTTGGAGGAAATCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCTCGTAATAAAAGATTGGATT
TCCCTTTG

FIGURE 76

MAVLAPLIALVYSPVRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFMSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIEFFANWSNDQSFQAPIYADLSLKYNC
TGLNFKGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCGGGACGTTGCCCTG
GGGCCAGCCTGGCCGGGTACCCCTGGCATGAGGAGAATGGCCTGTTGCTCCTGGTCCA
TTGCTCCTGCTGCCGGCTCTACGGACTGCCCTCTACAAACGGCTTACTACTCCAAAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGGAGACCCCTGTTACCCCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGGCCCTGGTCTCCCGCGCGTGTGCGTGTCAATGGTGGAAAGCT
GTGAGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT
TTGGGAGACTACCAAGGCGCGTGCACCTGCCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTCGGCTGGAGGACTATGGGCTTACCGCTGTGAGGTATTGACGGGCTGGA
GGATGAAAGCGCTCTGGTGGAGCTGGAGCTGCCGGGTGTGCTTACCAAGTCCCCCA
ACGGCGCTACCACTTCACGGGCCAGCAGGTCTGTCAGAGCAGGCTGCCGTG
GTGGCCTCTTGAGCAGCTTCCGGGCTGGGAGGGAGGGCCTGGACTGGTCAACGGGG
CTGGCTGCAGGATGCTACGGTGAGTACCCCATCATGTTGCCCGCAGCCCTGCCGTGG
CAGGCCCTGGCACCTGGCGTGCAGAGCTACGGCCCCGCCACGCCGCCCTGACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGGGGGGTGACTACCTGGAGCACCTGAGAAAGCT
GACGCTGACAGGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGGAC
AGCTTTGCCGCTGGAGATTCCATGCCCTGGACCGCTGCCACGCTGGCTGGCTGGAGAT
GGCAGCGTCCGCTACCCCTGTGGTTCACCCGATCCTAAGTGTGGGCCCCAGAGCCTGGGT
CCGAAGCTTGGCTCCCGACCCGAGAGCCGTTGTACGGTGTAACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCTGCCGATCCCTACTGGCTGTGATTTGAGTGGTT
CGTTTCCCTGTGGGTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTTC
TTAACATTTTTACTATTTGTAAAGCAAACAGAACCAATGCCCTCTTGCTCTG
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGGCATTGCGGTTGTGGCTCTG
GAGGGTTCCCGCCATCAGGCTGGTCTCCCTCTTAAGGAGGTTGGTGCAGAGTGGC
GGTGGCCTGCTAGAATGCCGGGGAGTCGGCATGGGGCAGATTCTCCCTGCC
CAGCTGGGGAGAGAGGGCCTGGGGCTCCGGAGCTGGCTTGGCCTCTCTGCC
CACCTCTACTTCTCTGTGAAGGCCGTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCCAAATCTGAGGGAGGAAGAAACTCCCTCCCT
TCCCTCTCGGTTCCAAAGAACATCTGTTGTGCTTGTGCTTCCCTGTG
GGAGGGGGCCCTCAGGTGTGTAATTGGACAATAAATGGTGCTATGACTGCCCTGGCAA
AA
AA

FIGURE 78

MGLLLVLVPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRLRHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGGCCATCCCCAGACG CAGGCCCTCATGGC
CAGGGGGAGGGTGCACCAGGCCGGCCCTGAGCGACGCTCCCATGATGACGCCACGGAA
CTTCCAGTACGACCATGAGGTTTCTGGGACGGGAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGGGGATCGGACCGCATGGACCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGCTGGATCGGCACACGCAGCAGCGCA
CATACGGGACTCGGTGAGCGCCGCTGGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCACTACGGCCGGTGAAGAATTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGGGGTTCCGGTGGC
CGACCAAGGATGGGACTCGATGGCACTCGAGAGGAGCTGACAGCCTTCTGCACCCCGAGG
AGTTCCCTCACATCGGGACATCGTATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCAGGTGGAGGAGTACATCGGGATCTGACTCAGCCGAGCTGGGAGGA
GGAGCCGGCTGGGTGCAGACGGAGAGGCGAGCTTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGCACTGGGTGCTGCCCTGCCAGGACGCC
CTGGTGGAAAGCCAACCACTGCTCACAGAGAGCGACACGGACAAGGATGGCGCTGAGCAA
AGCGGAAATCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCG
CACAATGACCGGAGGGGGCCGTGTTCTGGCCCTCCCTGTCCAGGCCGAGGAG
GCAGATGCAGTCCCAGGCATCTCTGCCCTGGGTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTCAACCCCCAACCCCAAGGGAGGGGCTGTCTAGTCCAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA
GAACCGCCCAACCCCTCCAGCTCAAATGAGCCTCCACACATAGACTGAAACTCCCT
GGCCCTGAGCCCTCTCTGGCTGGCTGGCAGACCTCCCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSDAGPHCQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDVSAAWDT
YDTRDRGGRVGWEELRNATYGHYAPGEEFHVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRSLKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCCTGCCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGGAGCCCCGG
GGCGCGGGCGGGTGCAGGGATCCCTGAGCCCTCTGTCCTGTTCTTGTCGCTCCCCAG
CCTGTCGTCGCTGCTGTTTGGGCCCGCCCTCCCGCGTGGCGGGGTTGACACCGATCTG
GGCTTCGCTCGATTGCGCGAGGGCGCTCCAGACCTAGAGGGCGCTGGCTGGAGCAG
CGGGTCGCTCTGTCCTCTCTCGCCGGCGCCCTCCGCACCTGGCGTGGGGCTCT
GAGGAGGTGACCGCGGGGCCTCCGCACCTGGCGTGGCGCATCTCCCTCTCTCCAG
GTGTGAGCAGCTATCAGTCACC**ATG**TCGAGCCTGGATCCCGGCTCTCGGCTCGGTGT
TGTCTGCTGCTGCTGCGCCGGGGCCCGGGAGCAGCAGGGAGCCGCTCCATTGCTATCACATG
TTTACAGAGGCTTGGACATCAGGAAGAGAAGCAGATGCTCTGCCCCAGGGGCTGCC
CTCTGAGGAATTCTCTGTCGTTGGAACTAGTATGCTCTGTCGAGCATATGTC
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACAGTCTAGCTACC
TGGTCGAGAAAACATTCTCAGTAGATGCGCATCCAGTCTCAATGCTTCTAGAT
GGTCGCTCTTACAGTAATTAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAAGCA
GTGTCCACAGCACATCCACCAACAGTAACAGACTAAAGAAAACACCCGAGAAGAAAAC
CAATAAAAGATTGTAAGCAGCACATTGCTTGGATGTTAAATTGGCAG
GCCGATTAAATTACAGAAAGATTGCTTGGCATTGATTGATGGAAGCTTTAATATTGGCAGC
GAAGGACACATGTGGCTTGTCAAGCAGTGAACATCCAAAATAGAATTAACTGTAA
AAACTTACATCAGCAAAGATGTTGTTGCTTGCATAAAGGAAGTAGGTTCAAGGGGGTA
ATTCCAATACAGGAAAGCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGTATTATGGATGGTGGCTTCTGATGACAT
CGAGGAAGCAGGATTGTCGGCCAGAGAGTTGGTGTCAATGATTAGTTCTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTAGCTGACATTTGTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTCTTCTTACACATGCCAACATGGTTGGCACCAAAATACGTAAA
GCCTCTGTAACAGAACAGTGTGCACTCATGAACAAATGATGTGCAACAGACCTGTTATAACT
CAGTGAACATTGCTTTCTAATTGATGGCTCCAGCAGTTGGAGATAGCAATTCCGCCCTC
ATGCTTGAATTGTTAAACATAGCCAAAGACTTTGAATATCTGGACATTGGTGCACAGAT
AGCTGCTGTAAGTTACTTATGATCAGGCCACGGAGTTCACTGACTATAGCACCA
AAGAGAAATGTCCTAGCTGTCACTAGAAACATCCGTAATGAGTTGGAGACGACTACTGGT
GATGCCATTCTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCTAGTAATTGTCAGATGGCAGTCTTGTGATGATGTCAGGGCTTGAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTTGGCTTGGCCTGGCACCTGAGATGACCTG
AAAGATATGGCTTCAAACCGAAGGAGTCACGCTTTCTTCAAGAGAGTTACAGGATT
AGAACCAATTGTTCTGATGTCAGAGGCATTGAGAGATTCTTGAATCCTCAGCAAT
AATGGTAACATTGACAACTGAGAAAAGTACAAGGGATCCAGTGTGAAATTGTTATT
CTCATAATACTGAAATGCTTAGCATACTAGAATCAGATAACAAACTATTAAGTATGCAAC
AGCCATTAGGCAATAAGCATTCTTAAAGCCGCTGCCCTCTGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCAATCATGGCTTCTAGAAAACCTCAGGAAAGAGGA
GATAATGTTGATTAACACCTTAAGAGTTCAACCAGCTACTAAATGTCAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATAGACCAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLPGAGSEGAAPIAI TCFTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRMLFEVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSTFDYSTKENVLA
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGACCCGGGGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCGGCCTCCCCGGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCACTCGTCCAGTC
GGGCGGGCGCTCGGGCGCAGAGGGAGATCGAGCGGCTTGGGGCACCCCTGCTGTGCC
TGCTGGCGCGCGCTCCCCACGGCCCCCGCTCCGACGGCAGCTCGCTCCAGTC
AAGCCCGGCCCCGCTCTCAGCTACCCGGAGGGAGGGCACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACGTAGGGAGGACAGCAGCACAAATTGCGCAGCGGGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAACTTACCTCCAGCTAT
CACAAATGAGACCAACACAGAACCGAAGGTTGAAATAACCATCCATGTGACCGAGAAAT
TCACAAGATAACCAACAACAGAACCGAAGGTTGAAATAAGTCTTTAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGGAGGAACAGACTGGACACAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTAAGTCCAGTTGCCAGCTTCCAGTACACCTGCCAGGCATGCCGGGGCAGAGGATGCT
CTGCACCCGGGAGACGTGAGTGTGCTGGAGACCGAGCTGTGTCTGGGGTCACTGCACCAAAA
TGGGACCCAGGGGAGGAACATGGGACCATCTGTGACAAACAGAGGGACTGCCAGCGGGGCTG
TGCTGTGCCCTCCAGAGAGGGCTGCTGTTCTGTGTGACACCCCTGCCGTGGAGGGCGA
GCTTTGCCATGACCCGCCAGCCGGCTTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGGCTTGACCGATGCCCTTGTGCCAGTGGCTCTCTGCCAGCCCCAACAGGCCAGGCTG
GTGATGTGTGCAAGCCGACCTTCTGTGGAGCGCTGACCAAGATGGGAGATCTGCTGCC
CAGAGAGGTCCCCGAGTGAAGATGGCAGCTTATGGAGGAGGTGCGCAGGAGCTGG
AGGACCTGGAGAGGGAGGAGCTGACTGAAGAGATGGCAGTGGGGAGGACCTGGCTGCCCGCT
GCACATGCTGGGGAGGGAGAGATAATTAGATCTGGACACGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTTCCCCAGGTGTGCTTAGGCGTGGCTGACCAAGGCTTCTTCTACA
TCTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCAATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTTCACTGCTGGCTGGAGAGTCAGGCGAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCCCTGTCAGATTATTGCTGCTTGGCTCTACCAAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTGATTGGTTTGGGAAATGTGAGAGAGATGGCAGTGGCTTGCACAAACATCAA
CTGGCAAAATGCAACAAATGAATTTCACGGCAGTCTTCCATGGCATAGGTAGCT
TGCCCTCAGCTGTGCAAGATGAAATGTTCTGTCACCTGCATTACATGTTTATTCA
AGCAGTGTGCTGCACTCCACCTCTGTGGCAGGGCAGCATTTTCAATCCAAGATCAATT
CCTCTCTCAGCACAGCTGGGGAGGGTCTATTGTTCTCTCGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGGCCCAAGTCACACAGCTAGTAAGGACAGAGCAGTTCT
CTGGTTGTGACTCTAAGCTCACTGCTCTCTCACTACCCCCACACCGCTTGGTGCACCAA
AAGTGTCTCCCCAAAAGGGAGGAGAATGGGATTTTCTGAGGCATGCACATCTGAAATTAG
GTCAAACTAATTCTCACATCCCTAAAGTAACACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGTCTCTTAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT
TGCATTAGTAATTGTAGGGCGAGGATAATGAATGCTGAGCGTAGCATACAGGTTAACCTGCA
GTACTTGTGAAATTGTAGGGCGAGGATAATGAATGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGTT
GTAATATGCGACTGCGAACACTGAAACTCTACGCCACTCCACAAATGATGTTTCA
TGGACTGTGCAACCATGTTATCATCCAGAGTTCTAAAGTTAACCTGCA
TAAGCATGCTTCTTGTAGTTAAATTATGTATAAAACATAAGTGCATTTAGGAATCAAGC
ATAAACTCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

FIGURE 86

MRLLVAPLLLAWAGATATVPVVPWHVCPQCACQIRPWYTPRSSYREATTVDCNDFLTA
VPPALPAGTCQLLQSNISIVRVDQSELGYLANLTELDSLQNSFSDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGKFLDLNKNPLQRVGPQDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFTHPRAFHLPQMETLMLNNNALSALHQCTVESLPLNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVVPEGTLELRRVTAAEEAGLYT
CVAQNLVGADETKTVSVVVGRAALLQPGRDEGGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLA AHLGTQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLWPWNPGRKLPSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

FIGURE 88

MRQTIIKVIKFILIICTVYVHNIKFVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSIDPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNNEWTLKDLRQLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI
YSLKTKLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELLELIRCDLERIPHISIFSLHNLQEIDLKDNNNLKTIEIIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNPKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRLAHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGTACTTGTCATGGAGCTGGCACTGCGGCCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCGTGCCTGGGCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTTATTGCAACCAACTCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGGCTTAGCAGTGGATTGGAAACTTGTGAGGAAATTGGGC
CCCTTGACAGTGTCTCAAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCTTATT
GTGGATAATCCCGTGGGCACTGGGTTCACTGGGTTCACTGGGTTCAAGTGAATGGTAGTGGTGCCTATGCCAAGGA
CTGGGCTATGGTGGCTTCAGACATGATGGGTTCTCTGAAGACCTTCTCAGTTGCCAACAAAG
AATTCCAGACAGTTCATTCTACATTTCTCAGAGTCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGAACATTGCGGGGT
TGCCCTGGGTGATTCTGATCTCCCTGTTGATTGGTCTCTCTGGGACCTTACCTGT
ACAGCATGTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGCTAAGGGTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACACTAAAGCAGCTCCA
CGTCTACAATGGAGTCAGCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTCAAGCGC
CACGTGAGACACCTACAACAGAGATGCCCTAACGAGCTCATGAATGCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTGAGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGATAATGGACAGCTGGATCTCATGCTAGATACCATGGTCAGGAGGCCTG
GGTGCAGAAACTGAAGTGGCCAGAACTGCCCTAAATTCACTGCAAGTGAAGTGGAAAGGCCCTGT
ACAGTGCACCTAAATCTTGGAAACATCTGCTTGTCAAGTCCTACAAAGAACCTTGTCTTC
TACTGGATTCTGAAAGCTGGTCAATGGTCTTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTCACTCAGCAAGAAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAAGCTTCTGACAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAAAACCTAAGATTGTTAAAAAAATTGAT
TTGTTTGTCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWL~~L~~LLP~~L~~LLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMF~~WW~~LYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGN~~EE~~IGPLDSL~~K~~PRKTTWLQAASLLFVDNPVG~~TG~~FSY
VNGSGAYAKDLAMVAS~~MM~~VLLKTFFS~~C~~KEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
G~~T~~IKCNFAGVALGDSW~~I~~SPVDSVLSWP~~P~~YLYSMS~~L~~LEDKG~~L~~AEVSKVAE~~Q~~V~~L~~NAV~~N~~K~~G~~LYRE
ATELWGKAEMIIEQNTDGVNFYN~~IL~~T~~K~~STPTSTM~~ESS~~LEFTQSHLVCLQRHVRHLQRDALS
QLMNGPIRK~~KL~~II~~I~~PEDQSWGGQATNVFVN~~ME~~DFMKPV~~I~~SIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWRKLKW~~PE~~LPKFSQLK~~W~~KALYS~~DP~~KS~~L~~ETSAFV~~K~~SY~~K~~NLAFY~~W~~ILKAGHMVP
SDQGD~~M~~ALKMM~~M~~RLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCA**TGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCT**
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCA**CTCGGGCGTTGGCGTGGCA**
GGGGAGCCTGCCCTGTTGGGATTCCACGTATCGGAGTGGCTGCTCAGGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGGCCCTGCACCTGGGAATTCAACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACACTAAACACATCCAGGCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCACACCCCTCAGGAAGTTCAAGGCCATATAAAACA
ACTCTATGTCAACCACCTCTCAAGTGACAGTTCCCAAGGACATCTTGGAGACATG
GTTTGTGCTGCCAACGCCAAGCGGGAGGATGCCCTGCTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAAGAACAGACTGTTGATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAG
CTGATGGCCAAGGTGGCATGCTCCAGCCAGCCCCCTCCTGGCCACTACTCTTTCCCTCT
TCTCTGGGCTCTCCACCTCTGGGCCGGT**TGAGCCTACCTGAGCCCATGCGCCTGGGC**
CACTGCCAAGTCAGGCCCTGGTCTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPEQEAAPLSGPCGRRVITSRIVGGEDAEELGRWPQGSLRLW
DSHVCGVSSLHRWALAAHCFETYSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLsapVTYTKH1QPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVLQVVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSVWVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGACCGCTGGGAAGGGCAGAATGGGACTCCAAGCTGCTCTAGGGCT
CTTGCCCTCATCTCTGGCAAATGCAAGTACAGCCGGAGCCGACCGGGAGGACG
TGCCCCCAGGCTGGGTGTCCTGGCCGTGGAGCCCTGAGGAAGAGCTGAGTCACCTT
GCCCTGAGACAGCAGAATGTGAAAGACTCTGGAGCTGGTGCAGGCTGTGCGGATCCCAG
CTCTCTCAATACGGAAAATACCTGACCGCTAGAGAAATGTGGCTGATCTGGTGA
GGCCATCCCAG
CACTGACCCCTCACAGGTGCAAAAATGGCTTGGCAGCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCCTGGCTGAGCATCGACAAGCAGAGCTGCTGCC
TGGGGCTGAGTTTCACTCAACTATGGGGAGACCTAGGAAACCCATGTTGAAGGTCCCAC
ATCCCTCACAGCITCCACAGGCTTGGCCCCCATGAGACTTTGTGGGACTTGAGGCT
TTTCCCCAACATCATCCGTAGGCAACGTCTGAGGCCAGGTGACAGGGACTGTAGGCT
GCATCTGGGGTAACCCCTCTGTGATCCGTAGAGATAACACTTGACCTCACAGACG
GCTCTGGCACCGAACATAACGCCAACGGCTGTGGCCAGTCTCGAGCAGTATTC
TCAGACCTGGCTCAGTTCTGGCTTGGCAACTTGCACATCAGGCATCAGTAGC
CCGTGTGGTGACAACAGGGCGGGGCGGGCGGGATTGAGGCCAGTCTAGATGTG
ACTGATGAGTGCTGGTGCAACATCTCCACCTGGGTCTAGTACAGTAGCCCTGG
GGACAGGAGGCCCTCTGCACTGGCTCAGTAACTGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGGCCATCAGCGGG
ACACTGAGCTCATGAAGGCTGCGCTCGGGCTCACCTGCTTGCCTCAGGTGACAGT
GGGGCCGGTGTGGTCTGTCTGGAGAACACCCAGTTCGCCCTACCTTCC
CCCCATGTACCAACAGTGGGAGGCAACATCTCCAGGAACCTTCTCATCACAA
TTGTTGACTATACAGTGGGTGGCTCAGCAATGTGTTCCACGGCCTCATACCAGGAG
GAAGCTGAACGAAGTCTGAGCTAGGCCCCACCTGCCACCATCCAGTTACTTC
CACTGGCTCAGTGGCTCAGTAACTTCTGATGCTACTGGGGTCA
GAGTCCCATTCCATGGGTGCGGAACCTCGGCCCTACTCCAGTGT
GGGGGGGATCTTA
TCCTTGATCAATGAGCAGACAGGATCCTTAGTGGCGCCCCCCCTTCTGG
GCTCTACAGCAGCATGGGCAGGTCTCTTGATGTAACCCGGTGGCT
TGATGAAGAGGGTAGAGGGCAGGGTTCTGGCTCTGGCT
GGGGAAACCAACTTCCAGTTGCTGAAGACTCTACTCAACCCCTGACCC
TTATCAGGAGATGGCTTGTCCCTGCCGAAGCTGGCAGTTCAGTCC
GAAGCCTGCTGAACCCCTCAATTGACTCTGCAAGACGCTTACT
TGTGTGAGCTTGTGACTTCACTCCCAACCTCATGCTCAT
ACTCCACTGGGATCTCTGCTTCTGGCT
AGGAGAGATGGCTTGTCCCTGCCGAAGCTGGCAGTTCAGTCC
GAAGCCTGCTGAACCCCTCAATTGACTCTGCAAGACGCTTACT
TGTGTGAGCTTGTGACTTCACTCCCAACCTCATGCTCAT
ACTCCACTGGGATCTCTGCTTCTGGCT
ATCTCATCTTCTCTTCACTAGGGCTTCTGGCT
TTCACTTGTGATATTCAATTCCCAACTTCACTGCAAGAGAC
CTCTGCTTCTGGCT
TTCACTTGTGATATTCAATTCCCAACTTCACTGCAAGAGAC
CTCTGCTTCTGGCT
GCCTTACCCATCATAGTTGCCCCACTCCCTCTTACTTAGCT
ACTACTCTTGCTCTCTCATCAATTCTGCTTCTCATGG
TCCATTGAGATTTTGCTTCTCAGTTACTCATTG
TCTACAACCAATTACCATCTCACTAAAGACTTT
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSFTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHGVTPSIRKRYNLTSDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAARGLTLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTVGGTSFQEPFLITNEIVDYISGGGSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPGWDPVTGWGTPTSQCL

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

Font: DejaVu Sans Mono

GGCGCGCGCTCTCTCCGGCGCCACACCTGTCAGCGGCGAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCTCGGC**ATGG**CAGGGATTCAGGGCTCTTCTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGTCGTCTGCCCCAGTCTACCCCAATTAGCCAAGCCAGACT
TTGGAGCGAAGCAAATTAGAAGTATCTCTTCACTGTGGACCCCAGTGTCTATGCCAATGG
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGCTTATGAAACGCTTATGCCAATGG
CAGCCGACAGAGACGCAAGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGACTTCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGACCCCTGGTGGCAGAGAAGCATGCTTCACAGTGCCCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCAGGGGCCAACGACTCCACTTCAGCCATGCCAGAGATGAA
ATTTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTTACAGCAATGCGATGCCAGCCAGGGGCCAGCGGGCTGGGTCTAT
GTGAGGATGTGAAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTGGCATTTTCAGG
GCACCACTGGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGCAAGATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGAACACAGTGTCCCTCTGGCAGCAATTAAAGGGCTTCATGTTTATTAGGAGAGGCC
AAATTGTTTTGTCAATTGGCGTGCACACGTTGTTGTTGTTGTTGTTGTTGTAAGGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATCTG
GTTTGTGATCATATCATATCATTTAACGAGTTGAAGGCATACTTTGCATAGAAAATAA
AAAAAAATCTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATCTTACGGTTTG
CAAACATTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATTTGCA
CAAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTE
TQVGIIYILSSSGDGAQHRDGS
SSGKS
RRKRQIYGYDSRFSIFGKDFL
LNYPFSTS
VKLSTGCTGTLVAEKHVL
TAACCIHDGKTYVK
G
TQKLRVGFLKPKFKDGGRGANDSTS
SAMPEQMKFQWIRVKRTHVPKGWIKGN
ANDIGMDYDYA
LLELKKPHKRKF
MKIGVSPPAKQLPGGRIHFS
GYDNDRPGNLVYRFCDV
KDETYD
LLYQQCD
AQPGASGSGVYV
VRMWKRQQQK
WERKI
IGIFSGH
QWV
DMNGSPQDFN
AVRITPL
KYAQIC
Y
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGGTCTCTCGAGCCTGCTGCCCTGCCCTCCCCGCCACCAGCCATGGTGGTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATCGGCCAGGGATACCTGTTCCCCAGCCTGTGGGAAGCCCA
GCAGCTGAACCGGGTTGTGGGCCGGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGCTGCTGCTGG
GCCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCAGAAGGTGGGTGTTGCCCTGGGTGGAGC
CCCACCCCTGTGTTCTGGGAAGGAAGGTGCTGTGAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCGGGCTACTT
GGAGGGGGAGCAGGGATGTTGCTGGGCGACTCCGGGGGCCCTCATGTGCCAGGTGGAGC
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAACGATGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCG
CCCGCGCGCTCTAAGGGCGCAGCGGGACCGGGCTGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGGCGGGCTCGGGCGTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCGGACGGCTGCGGAAAGGAAACCCCTCCCCGACCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCGCCAACGGCTCATGCCCCGCCAAC
GACTTCCGGCCCCGGCCCGGGCCAGCGCTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTTGTAACCCGCCACATATCTTATTCTCCAATTCAATAAATTATTTATT
CTCCAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
M V V S G A P P A L G G G C L G T F T S L L L A S T A I L N A A R I P V P P A C G K P Q Q L N R V G G E D S T D S E W P
W I V S I Q K N G T H H C A G S L L T S R W W I T A A H C F K D N L N K P Y L F S V L L G A W Q L G N P G S R S Q K V G V A
W V E P H P V Y S W K E G A C A D I A L V R L E R S I Q F S E R V L P I C L P D A S I H L P P N T H C W I S G W G S I Q D G
V P L P H P Q T L Q K L K V P I I D S E V C S H L Y W R G A G Q Q P I T E D M L C A G Y L E G E R D A C I G D S G G P L M C
Q V D G A W L L A G I I S W G E G C A E R N R P G V Y I S L S A H R S W V E K I V Q G V Q L R G R A Q G G G A L R A P S Q G
S G A A R S
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTGGAGCCCTCACAGATGAGGGAGAAACGTTGATGGT
GGAGCTGCACAACCCTACCGGGCCCAGGGTATCCCCGACGCCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCCTCGCCAAGGCTACGCACGGCAGTGCGTGTGGGCCAC
AACAGGAGCGCGGGCGCCGCGGAGAATCTGTTGCCATCACAGACGGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGCGGCCACTACAGCAGGGTGTATGGCCAAGACAGAGGGATC
GGCTGTTGGTCCCACTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATGAATTACT
GGTGTGCAACTATGAGCCTCGGGGAACGTGAAGGGAAACGGCCCTACAGGAGGGGACTC
CGTGCCCCAATGTCCTCTGGCTACCACTGCAAGACTCCCTGTGAACCCATCGGAAGC
CCGGAAAGATGCTCAGGATTGCTTACCTGGTACTGGACTCTGGACGGCCCATCTCCGGGGGACTGA
AGCATCAGACTCTAGGAAATGGTACTCCTCCCTGGACGGCCATCTGGACGGCCATCTGGACGGCC
TGGTAACAGAGGTCTCAGGCTCCCTGGACCCAAAGGCTGGCTGTGAAACCCAGGGCC
CCAACCTCCTTAGCAACGAAAAGACCCGGCCCCATGGCAACAGAGGGCTCCACCCTTCGGTAA
AACTGAGGTCCCCCCATTTGGCAGGCTGCTCACAGCCCTCCTTGGATGGAGGCAGTT
CCTCCCCAAATCGACCCATGTCCCTATCCAAATCAGCAAAAGGTGACAGAAAACAC
AAAGGTCCCTTAGGAGGCCCAGGAACCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACTCCTACCCCATGGCCAGGGAGGGCTGAGGCTGAGTTTGCCTCCTCAGGT
AGGTCTGGCTCAGGCCAGGACAGGCCAGGTGAGGCTGCAGGGCCACCTGGAC
CAACGGGGCAACCCCTCTCCAAGTCCCTGGCCAAATTTCCCCAAATACCTCTGGCCACGGCTAA
TGCCACGGGGCTGGCCGTCCCTGGCTCTGCAGGTCCCTGGCCAGGTGCAGGGGGCCCTGACA
AGCCCTAGCGGTGTCAGGGCCTGAACCTGGCCCTGGCTGTATGTGGGGCCCTCTCTGGGA
CTACGTCTCCGCCTCCCTGTGGATCTCTGTGAATGGGATACCACCTAAAGGG
TGAAAGGGGTCAGGCTGTCTCCCTGTCATTCCCCACCCCTGTCCCCAGCCCTAACAAGAT
CTTTGGTTAAGGCCCTCGGAGGGAAAGGCTACGGGGCAGTGCCTCATCACACCCATCC
ATCCCTGGAGGCCAAAGGCCCTGGCTGGAGGTCAGGAGGGCCCGCTGAGGAGGTCAACCC
GGGGCCCAACCCCTCCCTGGCCCTCCCTGTAGGTCCTTGGGGAGGATTGAGGGGAGCT
CACTGCCTACCTGGCCCTGGGGCTGTCTGCCCACACAGCAGTGCCTCTCCCTGAGTGGCCCT
TGTAGGCTGGGGATGGGGTTCCTAGGGGCAGAAGGGAAAGTAACCTCCGTACCTCCCAAAAAACCT
TTTGAGGTGGGGAGGGCAGGGAGGAAAGTAACCTCCGTACCTCCCAAAAAACCT
GTCCCAACCCGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFKAYARQCVGHNKERGRRGENLFAITDEGMDVPLAMEWWHHEREHYNLSAATCSPGQ
MCGHYTOVWWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGRPYQEGETPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAFPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELOQATLDHTGHHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVGWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413



Glycosaminoglycan attachment site.

amino acids 439-443



Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303



N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256



Amidation site.

amino acids 82-86, 172-176



Peroxidases proximal heme-ligand signature.

amino acids 287-298



Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138



Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172



FIGURE 101

GTAAGTCAGGGCTTTCAATTGGGAAGCCCTCAACAGAATTCTGGTCATTCTCAAGTTATGGTGGACGT
ACTCTGTTGTCCTCCCTGCTTTCACATTAGCAGACGGACTTAAGTCACACAGATTATCTTCAT
CAAGGCAAGTTCATGAGCCACCTCAAGGCTTCAGAGAGTGAAACTGAAACAACATGAATTGGAGACCATCC
AAACTCTGGGACCATCTGGCTTCTCTCTGAGGAGATGAAACTGAAACAATATTCTGGACCTTACGACCAAA
ACATCTGAAGATTCTAGTCCCTGAAACTTGGACCTTACGACCAAAATATTCTGAGGCTTACGAGCTCAA
ACTGCAAGCTTACAGCTCAAATATCTGTTACACAGCAACCGAGTCACATTAATGGAAACCTGGTATT
TTGGCCAACACACTCTGTTAAAGCTGAAACAGGAAATCTCAGCTATCCACCAAGATGTTAAACT
GCCCAACTGCAACATCTGAAATTGACCCAGGAAACAGGATAAAATGTAGATGGACTGACATTCAAGGCTTGG
TGCTCTGAAGTCTCTGAAATAGCAGAAAGGAACTGGACTAAGGAAACTCTGGATGAGCTTCTGGGGCTGAGCAA
CATGGAAATTGGAGCTGGACCTAACAACTTACAGGAACTTACAGGCTTACGGCTTGTGATGCT
GCAGGAACCTCATCTCAGGAAACAGGATCAGCCCTGAGCTGGGAGTTCTGGCAGAAAGCTCAG
TGAGGCTGACCTAACCTTCACTTACAGGTTAGATTGATTCAGGCTTCTGGCTAACGTTACTAAATAC
ACTGCACATTGGAAACACAGACTAGCTACATTGCTGATTGCTCTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAGAACATTTCTGGACTATTAGACAGATTAATGGCTTCTCTGGGCTTGACAAACTGTAG
GGGACTGATACTCCAGGAACTCGGATCTGGCTTACTAATAAAAGCCCTTACIGGTTGGATCATTGGAGCA
TCTGAGCTGACTGATCTCAGGAACTTACAGTCTTACAGGCTGATTCAACAGGATCAGTCTGGGAGTT
GCATTAAATACATCAAGCCTTCTGGCAGATTGGCAGCTAACAGTGGCTTACAGTGGGTGGCAGAACACTT
TCAGAGCTTGTAAATGGCAGTTGCTGCCCTACGGCTGCTAAAGGAGAGGATTTTGCTGTTAGCCAGA
TGGCTTGTGTTGATGATTACAGGAACTTACAGGCTGCTGGGAGAGCAGCTGATGCGAATAAAGGTT
CAATTGAGTTCTCATCTGCTCAGCTGGCAGCAGCTGATTCTCCAAATGACTTTGCTGAAAGAACATGA
ACTACTGCTGATGCTGAAATGGAAATTTGACACCTCCGGGCCAACGGTGGGGAGGTGATGGAGTATACAC
CATCCCTTCGGCTGGCAGGTTGAAATTGGCAGTGGGGATTAATCATGTTGCTCATCTCAACTTGGTC
ATCCACTACTGCTGAGATGCTTAACACCTTGGCAGTGGAGAGAACGCTGCGCTCAGTGTGATCCCCACTC
CGAGCTGGGGCATGGCAGCTGGGAGATGCTGCTGCTGGGGCCACCCAGATAGCCTGGCAGAAGGA
TGGGGGACAGACTTCCAGCTGACGGGAGAGCAGCTGATGATGCCAGGATGACGTGTTTATCGT
GGATGTGAAGATGAGGACATGGGGTATACAGCTGCAACAGTGGAGAATTTTACGGAAACTATG
AAACTCTGACTGCTCTGAAACACATCATTTTGGGGCCTCTGTTGGCAGCTGAAACTGGAAACACAGC
CGTCTCTACAGTCTGAGGAGGACGCCCTCCCTAAACTGAACTGAGGACAAAGATGATACCCCATTTGGTGT
AACCGAGAGGACACTTTTGAGCAGGAACTCAGCTTCTGATTATGGGACTCAGATGTCAGTGTGATGGAA
ATACACATGTGAGATGCTTAACACCTTGGCAGTGGAGAGAACGCTGCGCTCAGTGTGATCCCCACTC
CTGGGACTCTCTCAGATGACAGGGCCATCTGGAGATGAGGAGGGCAGTGGGGCTAGTGGGTGATCATG
CTGGGACTTGTGTTGTTGGGGCAGCTGCTGCTGGGGTGTGATCATATACACAGGGCAGGAGTGAAGA
TTGGCAGCTTACACAGACAGTGGGACTCTGGCTGCTTACAGGAACTTACAGGCTTACAGGAAAGCTT
AGCTGACAGGGCAGGATGGGACTCTGCTCTCAGAGAACTGGGACCCACCTTGTACATCTCAGGTGCTGG
ATTTTCTTACACACATGAGCTGAGTGGGACTCTGGCTGCTTACAGGAACTGGGACTTACAGGAAAGCTG
CAGACATGTGCTCTTGTGCTCTTGGGATCACAGGCTCTGACCTAGTGTGCTTACAGGAACTGGGACT
TCTGGGGACTTGTGATGAGGAAATGGGAAACACAGTTTAAACTGACCTATGAGCCAGTT
CATAAAGGAAAGGAGTCTACCCATGTTCTCATCTTCAAGAAGATCTGGCGAACGGAGCTTCAAGTAAATATC
GTGGCTTCACTGTGAGGAAACTTACACTAGTGTGAGGAACTTACAGTGTGAAACTTGTGAGGAAAGCTG
CTAAACAGTCTCTTGTGAGGAAACTCAGTGTGAGGAACTTACAGTGTGAAACTTGTGAGGAAAGCTG
TACCTCTGGAAAAGCTCTCAGGGACACTCACCCTAGATGCTTACAGGTTGGCAGCTGAGGAACTTGTGAGG
AAGGCTCTTGTGAGGAAAGCTCTCAGGGACACTCACCCTAGATGCTTACAGGTTGGCAGCTGAGGAA
AGATTTCTGGGAGGAAACTCAGTGTGAGGAAACTTACAGGAACTTACAGGAAAGCTTCAAGGACT
TTAGTACTTGTGAGGAACTTACAGTGTGAGGAAACTTACAGGAAAGCTTCAACTACTACCTCAAGTGA
AAAGAGAGAGGAAACTTGTGTTTAAATGGAGTTGAAATTAAAGGAAAAAATGCTTAAATTAACAGAT
GAACCAAAATACACAAAGGTTATGTTAAATGAGGAAACTTACAGGAAAGCTTCAACTTAAAGAAT
TTTTAACTTGTGTTATGCAAAAAGTATCTACGTAATTAAATGATAAAATCATGATTATTTATGTT
TTAAATGCCAGATCTCTTGTGAGGAAACTTACAGGAAAGCTTCAACTTAAACACCTGCTTGTGACCA
TTAAATAGAAGTACTTCACTTATATTGACATTATTTAAATAAAATGTGCAATTGAA

FIGURE 102

MVDVLLFLSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLEVKLNNNELETIPNLGPVSA
ITLSSLAGNSRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFALQLKYLQYLNNSNRVTSMEP
GYFDNLANTLLVVKLNRNRISAIPPKMFKLQLQHLELNRKIKNVGDLTFQGLGALKSLKM
QRNGVTKLMDFGAFWGLSNMEIILQLDHNNLTETIKGWLGYGLMLQELHLSQNAINRISPDAWE
FCQKLSLELLTFLNHLISRLDDSSFLGLSLLNLTLLHIGNNRVSYIADCAFGRGLSLKTLSDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNNRISITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSLLCDCQKWLPOWVAENNQFSFVNASCAGHQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAGQ
GEVMEYTTILREREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDDGTDFFPAARRMHVPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSSPPPPLKLNWTKDDSPLVVTER
HFFAAQGNQLIIVDSDVSDAGKYTCMNSLTGTERGVNVLRSVITPTPTCDSPQMTAFLSLDDG
WATVGVVIIAVVCCVVGTSLVVWVIIYHTRRRNEDCSITNTDETNLPADIPSYLLSSQGTLLAD
RQDGYVSSESGSHQFVTSSGAGFFLPQHDDSGTCHIDNSSEADVEAATDFFLCFLGSTGP
MYLKGNVYGSDFETYHTGCPDRTVLMHDYEPSYIKKKECYPCSHPSEESCRSFSNISW
PSHVRKLLNTSYHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLAHSSPDLSGSEEDGKERTDFQEEHICTFKQTLNEYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCAGTGAAGAGACTTTTTGGTGTGGCTGTGGGCTCTGGCAAAATG
AAGGATGCAGGACGCGAGTTCTCTGGAAACGGCAATGGATAACTGATTGTGCAAGAGAGAAGGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAATGTATATGTGACACAGGGAGCATCAAGAATGAAA
TAAACAGAGTGTAGCAGGGTTGGTGTGTTCTGACATAAAATTAATCTTAAGAGCAGCTGTCCTCC
CCACCCCCAAAAGAGATGTGGAAATGAAGACCGAGGATTCACAAAGAAAAGATGTGCTATTCTC
TATAAAGGAGAAAGTGTAGCAGGAGATAATTGGAAATGAAAAGTTGGGCTTTTTACTGAAAGTAAGA
GGTGTGGTGTGTTCTCTTGTGAAATTTCAGGAGAGGAAATTAAATAATCATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTGTGACCGCGCAGATTGAGGCATGTGTTGGGAGAGAACCGAGACAGTTGGA
TTTGCTCTATGTGACTAAATTCAGGATAATTGCACTGGATTCTTCATCAACCTCTTTTTTAAT
TTTATTCTCTTGTGATCAAGATCATCTGGTTCTTCAACCACTGGATTCTCATCTGGATGTGCT
GTGATCAGTGTGAAATACAACACTGTGTTGAACTCAGAGGACCAACACAGATAATTATGATGTGAA
GACCTTACATCCACAGATATGATGGCTCTAGTTAACAGGCCATTGGACCCCTGCTGTGGTGT
GCTGGCTCTCAACTCTGTGTTGCTGTGCGGCTCAGACCTGGCTCTGTGTCAGCAA
CCAGTCAGCAAGGTGATTGTGTTGGAAACCCCTGGCTGAGGGATGGCATCTCCACAAACACAGCGT
GCTGACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACACCTTCAGACATTGAGGACATTG
ACAGTTGACTGAGGAACTATCAGAAAGGATTGGGAACTTCAATGGCTTGGGAACTTCAACACTGTG
ACTCTTGACAACTGCTTACTACATCCGGATGGACTTTGTATACTTGTCTAAACTGAAAGGAGCTGTGTT
GGGAAACACCCCCCTGAAAGCATCTTCTTATGTTTAAACAGAATTCTCTTGGCCGACTAGACTTAGG
GGAAAGTGAAGAACCTTGTATCATCTCAGAGGCTGCTGAGGCTCTGCAACTTGGAACTTGTG
CATGIGCAACCTTCGGAAATCTCAACTCACACCGCTCATAAAATAGATGAGCTGGATCTTCTGGGAACTCA
TTTATCTGGCATCAGCCCTGGCTCTTCCAGGTTGTGCAAGCTTCAAAACCTGTGAGTATACAGTCCCAGAT
TCAGTGTGAGAACCTGTTGAGAACACTTCACTGGAGGATCAACCTGAGCAGACTTCAGCTG
ATTACTGCTCATGACTCTTCACTGGCATCTCACTAGAGCGGATACATTACATCAAAACCCCTGGAACTG
TAACTGTGACATACTGTGGCTCAGCTGGTGGAAAGACATGGGCCCCCTGAAACACAGCTTGTG
TAACACTCTCCCACTAAAGGGGGGGTACATGGAGAGCTGACCCAGAAATTACTTCATGCTATGCTCGGT
GATTTGGAGCCCCCTGAGACCTCAACTGCACTGAAGGCTGCTGCAACTTGGAACTTGTGAAACCTTGTG
CTCGACATCTGTATCTGGATTACTCAGGAACTGCTGACACATGGGCTCTGAAAGTGGGATCTCACATC
GCTCAGTGTGTACTTCAAAATTCACAATGTAACTGTGCAAGATACAGGAGTACACATGTTATGGTGA
TTCCCTGGGAATACTACTGTCTCAGGACCCCTGAACTTACTGAGCAACCAACTACTCTCTCTACTTTTC
AACCGTCACAGTAGGAACTATGGAACCGTCTCAGGATGAGGACCGGACCAAGGTAAACATGTGGTCCACCTC
AGTGGTGCAGTGGGAGACCAATGTGACCCCTCTCAGGACCCAGGACAGGTCAGAGGAGAAAACCT
CACCATCCCAGTGACTGTATAAAACAGTGGGATCCCAGGAATTGATGAGGTCAAGACTACAAAATCATCAT
TGGGTTTTGTGGCCATCACACTCATGGCTGCACTGATGCTGGTCAATTCTACAAGATGAGGAAGCAGC
TCGGAAACACATCACGCCAACAGGACTCTGGTAAATTATAATGTGAGATGAGATTACGGGAGACACCA
CATGGAAAGCCACCTGGCCATGCCCTGATCGAGGAGTGGACCCCTAAATCACTTACAACAAATCTCC
CAACCAACACAAACAGTTAACAAATTAATCAACACTGAGTCAACCTGAGTTACAGGTTACAAAAACAA
CTCTAAAGACAAATGTACAAGAGCTCAATCTAAACATTTACAGAGTTACAAAAACAAACATC
GACAGTTTATTAAGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTTTATTAAGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAGTGTCTTACAAAAAAACAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRQAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLENQIQIICKVNSFKHLRHLIELQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLLRRLDLGELKRLS
YISEGAFEGLSNLRYILNLMCNLREIPNLTPLIKLDDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPILHHLERIHLHHNPWCNCIDIL
WLSWWIKDAMPSNTACCACRNTPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVWDETTNVTTSLTPQ
STRSTEKTFITPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLCAVLGRAGRSDGGRRGELGQPSGVAERPCPTTCRCLGDDLCSCR
KRLARLPEPLPSWVARLDLSHNRSLFIKASSMSHLQSLREVKLNNELETTIPNLGVPSANIT
LLSLAGNRIVEILPEHLKEFQSLLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLVLKLNRRNRISSAIAPPKMFKLPLQLHLELNRNKKVNDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMELQLDHNNLTEITKGWLGYGLMLQELHLSQNAINRISPDWEFC
QKLSELDLTFNHLHSRLDDSSFLGLSLLNLTIHGNRNSYIADCAFRLGSSLKTLDDLNNEIS
WTIEDMNGAFSGLDKLRLRLLIQGNRIRISITKKRAFTGLDALEHLLSDNAIMSLQGNAFSQLMK
KLQLQHLNNTSSLCDCLQKWLQPQWVAENNPFQSFVNASCAPQLLKGRSIFAVSPDGFVCCDF
PKPQITVOPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRRAQGGE
VMEYTTILRLREVEFASEGKVQCVISNHFGSSYVKAALKITVNLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAAERERRMHVMPEDDVFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQC1AGGSSPPKLNWTKDDSPLVVTERHF
FAAGNQLLIIVDSVDSAGKTYCEMSNTLGTGERGNVRLSVIPTPTCDSQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYVGSDPFTYHTGCSPPRTVLMHDYEPYSIKKKECYPCHPSEESCRSFSNISWPS
WVGRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSPMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLAHKSSPDLDSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYLDLT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDAPPAGTMAQS RVL L L L L P P Q L H L G P V L A V R A P G F G R S
GGHSLSP E E N E F A E E E P V L V S P E E P G P G P A A V S C P R D C A C S Q E G V V D C G I D L R E F P G D L P
E H T N H L S L Q N N Q L E K I Y P E E L S R L H R L E T I L N L Q N N R L T S R G L P E K A F E H L T N I N Y L Y L A N N K
L T L A P R F L P N A L I S V D F A A N Y L T K I Y G L T F G Q K P N L R S V Y L H N N K L A D A G L P D N M F N G S S N V
E V L I L S S N F L R H V P K H L P P A L Y K L H L K N N K L E K I P P G A F S E L S L R E L Y L Q N N Y L T D E G L D N
E T F W K L S S L E Y L D L S S N N L S R V P A G L P R S L V L L H L E K N A I R S V D A N V L T P I R S L E Y L L L H S N
Q L R E Q I H P L A F Q G L K R L H T V H L Y N N A L E R V P S G L P R R V R T L M I L H N Q I T G I G R E D F A T T Y F
L E E I N L S Y N R I T S P Q V H R D A F R K L R L L R S L D L S G N R L H T L P P G L P R N V H V L K V K R N E L A A L A
R G A L A G M A Q L R E L Y L T S N R L R S R A L G P R A W V D L A H L Q L L D I A G N Q L T E I P E G L P E S L E Y L Y L
Q N N K I S A V P A N A F D S T P N L K G I F L R F N K L A V G S V V D S A F R R L K H L Q V L D I E G N L E F G D I S K D
R G R L G K E K E E E E E E E E E E E T R

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341, 477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493, 535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGACCTGCTCCGGCGCGGCCCTCGCGCTGTCTCCGGGAGGGCAG
CAAGTAGGGCGGGCGCGAGGGCTGGGGGTCTCGAGACCTCTAGGGGGCCCTCCCATCGGGGCCACCC
CAACCTGTTCTCGGCCCACTGCCCTCGGCCCAAGGGCGCTGCCAACATGGATTTCCTCGCGCTGCT
GCTGGTATCCTCGCTACTCGCAGGGGGCGCCGAGTTCGACGGGAGGTGGGCCAGGCAATAGTGTCTCGAT
TGGCTATGCTGTTATGGTGGAGGAGTGTACTGCTGCTGGGCTGGCTCGGCCAGTCTGGGAGCTGTCAAGC
TGTGTGCCAACAGATGCAAACATGGTAATGTAATCGGGGAAACAAGTCTCAAGTGTCTGGGATCTG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTCTGAAGGCCCGGCCCTGTAAGCAGGTGCTGAACACTTA
CGGCAGCTACAAGTGTACTGTCAGCGGATATGTCATGCCCGATGGTCTCGTCAAGTGCCTGACTCTG
CTCCATGGCAAAACTGTCAGTATGGCTGTGATGTTTAAGGACAAATACGGTGCCTGCACTGCCCATCCTCGCC
GCACCTGCGCTCGATGGAGGACCTGCTAGATGTGATGTTGCTAAGGAAGGCCCTCGCTAGATT
TAGGCAATGTGTCACACATTTGGGAGCTACATCTGCAAGTGTCTAGTATAAGGCCTCGATCTAGTATAATGGG
CAAATATCAATGTCATGACATAGAGAATGCTACTCTGGTCAAGTATCGAGCAGCTTGTGCTGATGTTATAA
CGTACGTGGGCTCTAACAGTCTAAAGGATAACAGGGTATGGACTGACTGTGTTGATATCTCCAAA
AGTTATGATGAACTCTCGCTGTTATCATGTTACCAAGGAAATGTTAACAGGTTGACACAGGGAAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGGCTCGGAACCCATATACTCCATCTCCTG
CAGGCCACTCTAACGCGAACACAAAGACCTACACCAAAAGGCCAACACAACTCTACCC
CCTGGCAACAGAGCTCGAACACCTCTACCCACCAAGGGCAACCCAGGACTGACAACACTTAGC
ACCACTGCGGAGCTACCTCGAGGGGATTACAGTGTGACACAGGGTACAGGAGACCTCAGAAAACAGGG
AGATGTTGTTGAGTGTCTGGTACACAGTTGATGACTGACTGACTGATGGGATGGATCAGGGAGAAAGAACAA
TGACTTGCACCTGGGAAACCATCTGGGAGGCCACAGGGTGGCAATATGCAAGTGTGCGCAAGC
GGGAGAACCTGCAAGCTGGTGTACTCTCTGGGCTCTCACTGGGAGCTGTGCTGTG
CAAGGTGAGGGCTGCACTCTGGCACACTCCAGGTGTTGAGGAAACACGGTGGCCACGGAGCAGCC
GGGAGGAAATGGTGGCCATGGCTGGAGGCAAACAGATCACCTTGGGAGGGCTGACATCAAGAGGAATCACA
AAAGATGTTAAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAACCCATTGATGTTCTCAAGTATGAAGGGTTGGCACAGAGGGTTGGGACCGACTG
TTCTCCATATGCACTAAAGAATGACAAAGAGGAAACTGGCTTGAAGACTGAGTATAAGGGACCAATTCTGGCAGG
GGCCATTGTTGAAATCTCTCATAAAAGAAGATGTGAAACATCTCAGTATCTCTCTCTTCTAAAGGTTAGA
TAAAAATTTGCTTAAAGATGTTAAAGATGTTCTACCCAAAGGAAAGTAAACAAATTATAGAATTTC
AGATGTTTGATCTACTAGTAGTATGCACTGAAATCTTGAAGTAAATAATTGGCAAGGCTTAATTGAG
CATTCCCTCTGACACTCTTAATGGAGGGATTGAAAGGGGAGGCCACAAATGCGAGCTACTGAATA
TCTCTCCCTTATGGCAATCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA
AGATATTGTTAGTACTCTCGATGTTGCTAGTGTGGGGTGGTTCTAGTGTGTTCTCATGTTAAAGGTAAAGCC
TTCTATTGTCATGGGATGATGTTCAAGATTTTTTTAAAGAGTCTCTCAAGGAACACAGTTGAGAG
ATTTCATCGGGTGCACTCTCTGCTGCTGTCAGATTGTTCTGGCTGCTGAGAAAGAGTGGCCCTGCC
ACACGGGAGACGCTTCCCTCACCTCATGAGTATGATTGAGTCTCTTATCAATTGGACTCTCCAGGTTCCAC
AAAGACAGTAAATTGGTAACATGAGTCAATGAGGAAATATGGCTGAGATCATTAACTGGTAAAGGCGAGGGCTGG
AGGGGGAAATAAAATCTAAAGCCTTGGTAACGGCGAAATATGGCTGAGATCATTAACTGGTAAAGGCGAGGGCTGG
TCCTTTATGGTCAATACTGCAACGCTGAAGATGAAAGGGGAAATAAATGAAAATTTC
TGATACTGGCAACTAAAGTGTGAGGAAAGTATCTAAAGTACTGTATACTCTGTTTAA
CTAAAATAAAATGTTAGTGTGGTTCCAAAGGCCTAAATAAAACAAATTGGTAAATAAAACACTGTTAGTAA

FIGURE 110

MDFLLALVLVSSSLYLQAAAEDGRWRPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GCS SALTCSMANCQYGCDVVKGQIRCQCPSGLHLAPDGRCTCVDVDECATGRASCPRFRQC
VNTFGSYI CKCHKGFDL MYIGGKYQCHD IDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYI PKVMIEPSGIHVPGNGTILKGDTGNNNWIPDVGSTWWPKTPYI PPIITNRP
TSKPTTRTPKPTPIPTPPPPPLPTELRTPLPPTT PERPTTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSVLVHSCNFHDHGLCGWIREKDNDLHWEPIRD PAGGQYLTVSAAKAPGG
KAARLVLPLGLRMHSGDLCLSFRHKVTGLHSGLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSEQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTTCCCTTGCACAGGTGCTGGCTCGGGGCTGA
AGGTGACAGTGGCATCACACACTGTCAGCGTCAGAGGTGACAGGCCCTCACCTACCGTC
CACTATGGCTTACACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCA
CACAAATGCCAAATACTTACTGGGCTCTGTAATAAGTCTGTTCTGACTTGGAAATACC
AACACAAGTTACCATGATGCCACCAATCCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTAAGGTCACACATCAGGAAATGGAACCTCTGCAAGTCA
GAAGATACAAGTCACGGTTGATGATCTGTCACAAAGCCAGTGGTCAGATTCTCCTCC
CTGGGCTGTGGAGTATGGGGAAACATGACCTGACATGGCATGTGGAAAGGGGCACTCG
CTACCTTACCATGGCTTAAATTAGGAGACCTGTCACACAGCTCCACCTACTCTTTC
TCCCCAAACAAATACCCCTCATATTGCTCCAGTAAACAGGAAGACATTGGAAATACAGCT
GCCTGGTGGAGGAAACCTGTCAAGTAAATGGGAAAGTGTATATTATGCCATATATTAT
GGACCTTATGGGATTCAGTGAATTCTGATAAAGGCTTAAAGTAGGGGAAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCTTGTGATTCTCATCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCTCGTTAGAAGTT
GCATCTGAGAAAGTGGCCAGAACATGGACTATGTGCTGTGCTTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAATCATGTACACCTTCTAGCAAGTATAACTGGAAATATCACTATTGATT
ATATCCATGTGTTCTCTTCTATGGAAATACTCAACCTTACAACAAACTTATAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAATAACAGGAAGTCACAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTGGAAATATGATATTGTTGCTTCCAGATGTTCTGGTGTTCAGG
ATTCAGCAGGCTGTGTCAGGCCCTCTGATGTGATCGGGCAAGGATTGCAACTGACTAGT
GTATGAAGTTTACAGCACATCCCTGCCAGCAGCAAGACATCCAGAGTGAACCTTCTGG
GCTAAACAGTACATTGAGTGAAAATTCTGAAGAAACATTTAAGGAAAACAGTGGAAAAGT
ATATTAACTGGAATCAGTGAAGAACCCAGGACCAACACCTTCTACTCATATTCTTACA
TGCAGAACTAGAGGCCAGTGGAAATTGAACTTCAGCAGGTTTTCAGCATAACACAATGCTT
GTGCACAGAAAACATGTGGGAAATATTCTCACTGGAGACTCGTCTCATGCTGACGG
GGAGAACGAAAGTGCACAGGGTTCTCATAGTTGTATGAAATATCTCAACACCTCA
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCCTGCTCACCTACAAA
TGTTGAAACTTACATTGTTGCAATTGTTCACTTCAAAATTCTATCTGTTATTGACAA
TTAAGAATGCTAAATTATGTTCAATTGTTCAAAATTCTATCTGTTATTGACAA
CAAAGTAATAAGGATGGTGTCAAAAAACAAAACATGCTCTCTTTTTCAATCACC
AGTAGTATTGGAGAGACTGTGAACACTAAGGAATGACTATTAAAGCTTATTGTTA
TTTTTCAAGGAAAGATGGATCAAATAATTCTGTTGCTTAAAAAAAAAAAAAAA

FIGURE 112

MWNLKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPNAsLLINPLQFPDEGNYIVKVNIQGNGTLsAsQ
KIQVTVDDPVTKPVVQIHPGSAVEYVGNTLTCVVEGGTRLAYQWLKNGRPVHTSSTYsFs
PQNNTLHIAPVTKEIGNYsCLVRNPVSEMEsDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAIlFDCsADsHPPNTySwIRTDNNTyIiKhGPrLEVASEKVAQKtMDyVCCAYNNIT
GRQDETHFTVIITSVGLekLAQKGKSLsPLASITGisLFLiSMCLLFLWKKyQPyKViKQK
LEGRPETEYRKaQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPsRSVPASDCVSGQDLHSTV
YEViQHlPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCGGGAGTCAGTCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTCCTCGGACCCACGGCGGACCAAGCTGGCGTCACTACGGACAGA
ACTGGAGAGAAGTCTGCGGAAAGGAGACTGGATAGAATTATGCCCCGTGGCCTGCT
TGTCAAATCTCAACCGGAATGGGAAAGTTTGTCAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATCTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCTACTATTATCTGTAAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTAATAGTCAAAGTGGAAAGTATTGAGGCCGTTCATCATG
GTTTGGTCCAGGTTCTGATGAGTAGTATGTCAGCACTTTCACTATCATGTTGGA
TCAGGACGTCCTAACTTTATGGAAACCTTGGGATTCAGGTGAGGGATCATACT
GTTTTGCTTGAACACTGTTTCCGGACTTTAGGACTCTGTATGATAATTGTC
AGATTGCCCTTGCTTCAAAAGCGCAGACACGCCATACCCATACCCCTCAA
TATTATCAGAACTGTCACAAACCTTGGAAAGAGTGGAGGAGAACAGGGCGGATGAGAA
GATGTTTCAAGAAGAAGCTGAAAGTAAAGAACAAACAAAGACTTTCCACAGAATGC
CATAAAGACAACGGCTCTGGGCTCATTTGAGCAAGATAATCTAGTAAATTATAG
TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCATTGGTTGGTTGAAGTG
AACTGTGACTTTTGATATTGCGAGGGTTAGTCTAGATTGTCATTAAATTGAGACTCTA
CATTCAAGAACATAAAAGCAGTACTGGTATAACAGTTGAAATATGATTAAGCACAGTATGATG
GTTAAATAGTCTCTAATTGTTGAAAAATCTGTGCAAGCAATAAGATTATGATATTG
TTAATAAAACCTATTCAAGTCTGAGTTGAAATTACATTCCAAAGTATTGCTT
TGAGGTTATTAGAAGATTATTAGAGAAAATATTCTCATTGATATAATTTCCTG
TTCACTGTTGAAAAAAAGAAGATAATTCCATAAAATGGGAGTTGCCATTGTC
AAATGTGTTTCACTGACAAATTCTGGTCTTTAGGGTATATTCCAAAATTTCCTG
ATTTTAGGTATGCAACTAAATAAAAACACTTCCATTAATTAAATTCAAGTTCTACACA
GGTAAATACAGGATATGCTACTGATTAGGAGTTTAAAGTTCATGGTATTCTGTGATT
CAACAAAGTTGATTTCTCTGTATTTCCTACTATGGGTTACATTTTTATT
CAAATGGGATGAACTTGGAAACATTTTATGTTGAAACAGTATTGTT
GTTCAAAACTGAAGTTTACTGAGAGATCCATAAAATTGACAAATCTGTTGTAATT
TTGCCACTTTTCAGATTTCATCACTTGTGAACTCAACTGAAATTGTTTT
TTCTCTTTGGATGTTGAGGGTGAACATTCTGATTTCCTGATGTT
TTTACATTTCAGAAAGCTTAATGTTGCTCATATACAGAAAGTCTTAATGAT
TTTACAGTCGTAAATGCTTGTATTTAAATAACATTTTATATT
AAAGACAA
ACTTCATTAATCTGTGTTCTTCTGACTGGTAATTGTTGAGGGATTTCACAGTAAAA
GTCAGTAGGATGGAACATTAGTGTATTTCCTACTCTTAAAGAGCTAGAAATACAGTTT
CACCTTAAAGAGGGGGAAATCATAAATACAATGAATCAACTGACCAATTACGTTAGAC
AAATTCTGTAATGCCCCCTTCTCTGAGGCTCTGTTGCTGTGAATCATTAGATTACAG
TATGCTAATATAACAGTTCTTAAAGCCCTCTCTTAGAATTAAAATATTGAC
AAAGAGTTGGATGTTGTAACTTGTGATGCCCTAGAAAATCTAAGCACAAATAACCT
TTCTAACCAACTCATTAAAGCTGAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSMSMALSQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKGDFPQNAIRQRSLGPSSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GGAGTGTCCAGCTGGGAGACCGTGATAATTCTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAAGAGCGGG
AAGTCCTGCCAGACGAGCTGTGACACTTCCCTGTGACCATGAAACTCTGGGTGCTGC
ATTGCTGATGCCCTGGTTGGTGTGCTGAGCTGTGTCAGGCGAATTCTCACCTCTATTG
GCCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATAAAGAGCTGGCCAACAAAATGGAAGGCCCTGAC
TAGCAAGTCACTGCTGATGCTGAGGGCTACCTGGCTACCCCTGTGAATGCCCTACAAACTGG
TGAAGCGGCTAACACAGAGCTGGCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATCCTGCAACCTCTGTGAGCGGCAGTTCTTCCCCTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGTAGAGACTTCAAGGACACATACAGGCTGGACCCAGCACAACTTCCA
GAGGGGAACTTCAGGAACCAAGTACCAAGGCAATGCTGAATGTTGGATGACTGCTTGGATG
GCCGCTCGCCCTAACATGAGGGACTATTATCATACGGCTTGTGGATGAGCTGGTCT
AAAGCAGCTGTGATGCCGGGGAGGGAGGCCAACAAACCAAGTACAGGGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCGCCGCTGCTC
TCCCTGACCCAGGCAACAGAGCTGGGAGGAACTTCCGGTACTTTGAGCAGTTATGG
GAGAGAGAGAGAAAAAACGTTAACAAATCAGACAGAGCTGAGCTAGCAACCCAGAGGCA
TCTATGAGGCCCTGGACTACCTGCCCTGAGAGGGATGTTACGAGAGCCTCTGCTTGG
GAGGGTGTCAAACGTGACACCCCGTAGACAGAAAGAGGCTTTCTGTAGGTACCAATGGCAA
CAGGGCCCCAACAGCTGCTCTCCCTCAAAGAGGAGGACGAGTGGGACAGCCCCACAC
TCGTCAGGACTACAGTGTCACTGCTGTAGGAAACTCGAGAGGATCAAGGAGATCGAAAAA
CCTAAACTTGCACGAGCACCGTGTGATCCCAAGACAGGAGTCTCTACTGTCGCCAGCTA
CCGGTTTCCAAAAGCTCTGGCTAGAGGAAGATGATGACCCCTTTGTGGCCCGAGTAATC
GTCCGATGAGCATATCACAGGGTAAACAGTAAAGACTGCAAGAATTGTTACAGGGTGC
TATGGAGTGGAGGACAGTATGAAACCGCACCTCGACTTCTCTAGGGCACCTTTGACAGCG
CCTCAAAACAGAGGGAAATAGGTGAGCAGCTTCTAAACTACATGAGTGTAGAGCTG
GTGGTGCACCGCTTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGTGTG
TTCTGGTACAACCTCTGGCGAGCGGGAAAGGTGACTACCGAACAGACATGCTGCC
TGTGCTTGTGGCTGCAAGTGGCTCCAATAAGTGGTCCATGAAACGAGGACAGGAGTCT
TGAGACCTTGTGGATCAACAGAAGCTGACTGACATCCTTCTGTCTCTCCCTTCTGT
CTTCAGGCCATGTCACCTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGGACTCTGT
GTGACTGAAGTCCCAGCCCTTCATTCAAGCTGTGCACTCCCTGCCAACGGCTAGGATCA
AAGTGGCTGCAGAGCTAGCTGTAGCCCTAGCAAGGTGCTTGTACCTCAGGTGTT
TTAGGTGTAGAGTGTTCAGTGACCAAAGTCTGATACCTTGTACATGTTGTTTAT
GGCATTTCTATCTATTGTGGTTTACCAAAAATAAAATGTCCTTACAGGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVVEAKLSKIKSWA
NMKEALTSKSAADAEGLAHPPNAYKLVKRLNTDWPALEDLVLDQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDPTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLQDYLQSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEREKLTQNQTEABLATPEGIYERPVVDYLPERDVYESLCRGEVGVLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYVYDVMSEIERIKEAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYVGQQYEPHFDFS
RRPFDSGLKTEGNRLATFLNQYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYS
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPVYRDPNPKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVSHGDERPAWLMSETLRHLHHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSRLLLRLRPHLDGCRG
DILSARPDEWLGRCLLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGS SAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQI RNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAKPCPQLQGASRADVGADETALEQLNRRYQPLRFQKQRLLINGYR
RDPARGMEYTL DLLLECVTQRGHRRALARRVSLRPLSRVEILPMPYVTEATRVLVLPLL
VAEAAAAPAFLEFAAANVLEPREHALLTLVVYGPREGGRGAPDPFLGVKAAAAAELEERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPGGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

TOP: 5' → 3' BOTTOM: 3' → 5'

CGGAGTGGTGCACCGTGGAGAGGAACCGTGCCTGGCTGCCTTCTGTCCCCAAGCC
GTTCTAGACGCCGGAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AACGATTTCTGCTTGTACTATGCTAGGACACATTAGGATTGGTATGGAAATAGAA
TGCACCAACATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTC
GAGGATGAGCGCATGGAGCTAGTAAGAGCTTCAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAGGAGACTTGACCAAAACACTGTGACAAGCAG
AGTTCTCAGTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAATG
GTTCTCCTTGACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTTGTTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGAATTGCTTAAGTGTAGAATCAATGAAAAGACTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAGATATCTGAAGATAAAC
AGCTAGCAGTTGCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGTTCTATTAAAGAGGCAATGACTTACCC
CAACCAGGTAGTAGAAGGCTGTTGTTAGATATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGTATACGCCCTTAGGGCATTTGGCATTTTCAT
GATGCATTGGTTCTTACCTCAAATGGTCTGACAATGACTAGAAGTGGTAGAAAGCG
TGAATATGATCTTGATAGGACGTGTTGCTATTGTTGAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTTCTAAATTGGTGGCACTGGTATAACCACACATTAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTTAAACACATGAACATTGTAATG
TGTGGAAAGAAGTGTAAAGAATAATAATTGCAAAATAAACTATTAAATAATTTAT
GTGATAAAATTCTAAATTATGAAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT
AAAAAAATTAAAGGTCTTAGCGTCTAAGGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAGTAAACCTTTAGCTGTGTTCCCTTACTCTAAACTGATTATGTTCT
AAGCCTCCCCAAGTTCAATGGATTGCTCTCAAAATGTACAACAGCAACTAAAGAAA
ATTAAGTGAAGTTGAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRILNSLLNIPEKCPHQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNVQVVGCCSDMAVTTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAGAAAAAATGAATTCTAAATCAT
CTGAAACACAATGCACAGAGAGGATGCTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCTTCTAGTGCCTTTCATCACCAGATGTTGACATTCCAT
CTTCAAACTGTGATGAGAAAAAGTTCACTGAGAATTTCACAGAGCTCCTCGT
ACAATTATGGATCAGGTCAGTCAAGAATTGTTGTCATTGAACTGGAATTTCATCC
AGCTGCTACTCTTTCTACTGACACCATTCTGGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGCTCACCTGGGGTATCAACTCACAGGGAGCAGGAATTCTTCTACAAGA
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCAGGGTGTGAGGGTCAAG
TGGGTGGACGGCACACCTTGACAAAGTCTGAGCTCTGGGATGTAGGGAGCCAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTCGGATTGTGAAATGGTAGGAATAATCTTGT
AACAAAGGAAAATCTTAAAGAACAGAAGGCACAACCTCAAATGTGAAAGAAGGAGAGCA
AGAACATGGCCACACCCACCGCCCCACAGAGAAATTGTCGCGCTGAACCTCAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAAATAAGTAGTTAAATGTTAAAAAAA
AAAAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLLTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGTCGCCGTGGCCCTCAGCAACCCCTGCACATGGCGCTGAGGCCGCCACCGCGAC
TCGGCTCTCGCTCGCTGCCTGACTCTCTCTGCTGCTGCTTTCAGGGCTCGCTGATAGGGCTGTAACTC
TCAAATCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGATGAGACTGCTCTGATCATTCAGGATTCCG
AGACAGTGGAGACTGGGGCGGGTGTGCAAGAAACTCTGGGAAGACAAACACATATGTTTTTGACAACAAA
TTTGGAGACTTGGGGCGGGTGTGCAAGAAACTCTGGGAAGACAACTCCGAAAGATCTGAGATGTGACACGGAG
ACTCAGGGCTTATCGCTGAGGCTGGTCTGAAAGAAATTGATGAGATTGTGATCGAGTTAA
CTGTCAGGTAAGGACAGTGGGGCCACCCCGGCCATACAGCTGGTATGCCATGTGTAACACTGCCACGGATT
ACTGCCAGGAGACTGGGGCCACCCCGGCCATACAGCTGGTATGCCATGTGTAACACTGCCACGGATT
CCAGAGCAATCTCCAGATTTCCGAAACTCTCCACTTCAAGGACTTGGGTGTTCAGTGCCTG
TTCAACAGGACACTCTGGGCACTACTGCACTGGTCTTCAACAGGACTTGGGTGTGAGGAGCAGG
AGATGGAAGTCTGACCTGAAACTGGGGGAAATTGGGGGGGTTCTGGTCTGCTGTACTGGGCTG
TCACGGGGCATCTGCTGTCATCACAGCTGGCTTCAACAAATAACAGGATGAGAAAATTCAAGA
ACCCAGGGAAACAGGATGTTAACATACATCCGACTGACCGAGGAGGGCAGTTCAGACAACTGCTT
TGATCTGAGCCGGTGTGGCTGAGGCGCACAGGCGCACAGCTGACATACCTCTGCTGAGAAACTCTGTCAA
GGCAGGGAGACTGAGCTGACTCGGACAGCTGACACTTCAAGGAGCTTTGGGCAAAAGTGTGACCA
CTACTCTCTTACTCAAACAGGACATGAGAACTGGGGGTTCTGGTCTGCTGAGGACCCGGTAAATAACACCAA
GGAGGCGAAACTGGGGTGTGCACTGAGTTGGGTTCTGAAACTTGGGCTGATTCACAGGATTTAGG
GTGATCTTAAAGGAGTTGGCTACGCTAACCGCCGTGCTGGGGCCCTGGTGAAGGAGCATGTTACCAACTGTCGTT
CACGCCACGACGACCCATGTGAGATGCCAGGCTGGGACAGCACAGCGCATCCGGGGGACCCA
GAAAAGGCTCTTACACAGCAGCTTACTCGGCCACAGACACCCAGTCTTCTTAAAGGCTCTG
TGATCTGCTGAGTGGCAGTGTGCTTCACTGGAGGCTTGGGATCAGCATTTGGGCTGAGGAAACCTCTGGAG
GTAATTTGGGTTGCTGGAGGAGGATCTGGCTGAGGACCCCTGGTCTGGCAACAGGGTCTGAGGATTTAGGAAA
ACCTGCTCTTGGGCTGAGTGTGAAATGTTGACTGAAATATGTTCTTCTGTTTATTTAACTGTAATAATATTG
TACATCTAAATTGTTGCTAGGTGATTTGATTGATTTGAAAGAAAATTCTATTTAAACTGTAATAATATTG
CATACAATGTTAAATAACCTATTTTAAAGGCTCAACTTAAGGTAGAAGTTCAAGCTACTAGTGTAAAT
TGGAAAATCATATAATTAAGGATTTTACCAAGGAACTCTCTGATGAGATTACTGCTGATGTTCTCTTCT
CACACAAGTGGCTTACAGGCTTCTTCAAGGGAACTCATAGTCTGACTCATACATGAGCATTTCTTAAAGGCTCTG
TAAATAATCTGAGTGGCTGAGTGGCTTCACTGGAAACCTCTCAGGTTAGGTTGA
GCCTCTCTCTGAGATGACTGGAGCAGTGTGACTGGTCTGGCTGAGGACCCCTGAGATGACATACAGATG
CCAGTCAGTCCTGGGGTTCGGCCAGGCCCGCCTAGCTCAGTGTGCTGGCTGCTGCAAGGAGGCC
GCCCATCTGGGGCTGGAGTGGCTGAGCTGGCTGAGGAGCAGTGTGCTGGCTCTGAGGACACAGC
CTCTAGGGGGACTCGAGGAGCAGTGTGCTGGCTGAGGAGCAGTGTGCTGGCTCTGAGGACACAGCCT
TTTGGGTTAGGGCTGACAAATAGGGCCCAAACTGCTATTTTTTTTAAAGGTTGTTAAATTATTGTT
AAAGATGTCATAAGGCGAAAGGCAATTGCGAAATCAAGGCTGTCAGTACAAATAACATTTTAAAGAAAATGGAT
CCCACTGTTCTCTTGGCCACAGGAAAGCACCCAGACGCCACAGGCTCTGCGCATTTCAAAACAAACCATGAT
GGAGTGGGGCGCCAGTCCAGTGGCTGAGGAGCAGGCTGGGAGGAGCAGGCTGGGGGGAGGAAAAG
TGAAGGCGCTGATCAAAAGCAGTTTCAATTGACTTTAACTTTCATCGCCGGAGACACTGCTCCT
TGTGGGGGGACATTAGCAACACATCACTCAGAGGCTGTTCTCAAGAGACAGGTGTTCTGAGCTCAGCCT
GCCGCTGGACTCAGGACTGAAGTGTGTTAAAGCAAGGAGCTGTCAGGAAAGGAGCACTCAGTGTGCTG
GAATGGCTCTCACTACTCAGCTCCCTGTTCTGCTGCTGCTGGTTTTATACCTTGACAGTTTTTT
AATTGCTACATGAGACTGTTGACTTTTTAGTTATGTTGAAACACTTGGCCACAGGCCGCCCTGGAGGCA
GGAAATGCTCCAGCAGTGGCTAGTGTCTCCCTGGTCTGCTGAGTGGATCTGGCTCAGGCTCAGCCTCT
CTCTCCATCTGGGACCCCTGGTGAAGGAGGATGGCTCCCAACCTCTGAGGTTGGGGATTCAGGCTCAGCCTCT
TCTGGGTTGTCAGTGTAGGGTAGCTTATGGCCCTCTTCTTATACCTTAAACCTTCAACTACTG
TGGGAACAGGCTGAAAAGTAGAGAGAACTGAAAGTAGAGCTGTTGGAGGAGTAGCTGCTATAAACTGAGACTAGA
CGGAAAAGGAAACTCTCTGTTATTAAAGATGAAATGTTGACTCAAGACTCGAGGGCGATAACAGGCTG
GCCCTTGGATGGATGTTGCTGACAGATGCTACAGACTGCTACAGACTTGTACTAACACACCGTAAATTGGCATT
CTCATTATAAAAGCTTCAAAAAACCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDQEQTYYVFFDNKIQGDLAGRAEILGKTSKIKWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIA SNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGIICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267